

GenCore version 5.1.6  
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# OM nucleic - protein search, using frame\_plus\_r2p model

Run on: May 28, 2005, 15:38:35 ; Search time 90 Seconds  
(without alignments)  
5586.539 Million cell updates/sec

Title: US-09-869-566-4  
Perfect score: 1134  
Sequence: 1 taactcaccatgctgcact.....cgactcagagatcccgcg 650

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

MODE=frame\_r2p.model -DEV=rlp  
-O=/cgn2\_1/USPTO.epool\_p/US09869566/runat\_27052005\_163130\_19900/app\_query.faeta\_1.839  
-DB=A.Geneseq\_16Dec04 -QFMT=fastlan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09869566@CGN\_1\_154\_@runat\_27052005\_163130\_19900 -NCPU=6 -ICPU=3  
-NO\_WMAP -LANG=QUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -IONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

1: A.Geneseq\_16Dec04:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038:\*  
7: geneseqp20038:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1059	93.4	203	AA96933 Human IL-
2	906	79.9	192	AA95297 Human int
3	906	79.9	192	ADN05880 Actipsoi
4	902	79.5	197	AA95300 Human int
5	895	78.9	198	AA885138 Interleuk
6	895	78.9	207	AA96938 Human IL-
7	895	78.9	218	AA970927 Human z11
8	895	78.9	218	AA91885 Primate i
9	895	78.9	218	AA95299 Human int
10	895	78.9	218	AA96940 Human IL-

11	895	78.9	218	3	AA828266	AA828266 Human int
12	895	78.9	218	4	AA847186	AA847186 IL-1 rela
13	895	78.9	218	4	AA668116	AA668116 Human int
14	895	78.9	218	4	AA885136	AA885136 Interleuk
15	895	78.9	218	8	AD788306	AD788306 Human int
16	895	78.9	218	8	ADL15868	ADL15868 Human int
17	895	78.9	218	8	ADN05012	ADN05012 Antipsoi
18	895	78.9	218	8	ADN41836	ADN41836 Antio aci
19	895	78.9	218	8	AD004679	AD004679 Human int
20	892	78.7	218	8	AA971084	AA971084 Human z11
21	892	78.7	218	7	ADH89067	ADH89067 Human z11
22	891	78.6	218	3	AA970933	AA970933 Human z11
23	891	78.6	218	3	ADH89075	ADH89075 Human z11
24	885	78.0	193	3	AA96934	AA96934 Processed
25	885	78.0	193	4	AA887596	AA887596 Human PRO
26	885	78.0	193	5	ABG5921	ABG5921 Human sec
27	885	78.0	193	6	ABU90946	ABU90946 Novel hum
28	885	78.0	193	6	ABO34005	ABO34005 Human sec
29	885	78.0	193	6	ABU72022	ABU72022 Novel hum
30	885	78.0	193	6	ABU71576	ABU71576 Human sec
31	885	78.0	193	6	ABU91030	ABU91030 Human PRO
32	885	78.0	193	6	ABO27351	ABO27351 Human sec
33	885	78.0	193	6	ABU92546	ABU92546 Human sec
34	885	78.0	193	6	ABU81216	ABU81216 Human sec
35	885	78.0	193	6	ABO53330	ABO53330 Novel hum
36	885	78.0	193	6	ABU98333	ABU98333 Novel hum
37	885	78.0	193	6	ABU89338	ABU89338 Novel hum
38	885	78.0	193	6	ABU82545	ABU82545 Novel hum
39	885	78.0	193	6	ABU96509	ABU96509 Human PRO
40	885	78.0	193	6	ABU72179	ABU72179 Human PRO
41	885	78.0	193	6	ADB17199	ADB17199 Human tra
42	885	78.0	193	6	ABO44309	ABO44309 Human sec
43	885	78.0	193	6	ADA20004	ADA20004 Novel hum
44	885	78.0	193	6	ADB17387	ADB17387 Human tra
45	885	78.0	193	6	ADA20176	ADA20176 Novel hum

## ALIGNMENTS

RESULT 1	AA96933	standard; protein; 203 AA.
ID	AA96933	
AC	AA96933;	
XX		
XX	31-OCT-2000	(first entry)
DE	Human IL-1RA fused to heterologous signal sequence.	
XX		
KW	hIL-1RA; human interleukin-1 receptor antagonist-1; IL-1IP; osteopathic;	
KW	interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;	
KW	anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;	
KW	dermatological; immunomodulatory; gastrointestinal; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	Peptide	1..15
FT	Peptide	/label= Signal_peptide
FT	Peptide	16..23
FT	Peptide	/label= Flag_tag
FT	Peptide	24..36
FT	Peptide	/label= Linker
FT	Protein	37..203
FT		/label= hIL-1RA1
PN	WO2000039297-A2.	
XX		
PD	06-JUL-2000.	
XX		
PF	22-DEC-1999; 99WO-US030720.	
XX		
PR	23-DEC-1998; 98US-0113430P.	



CC nitric oxide synthetase, and metalloproteases, and upregulate and/or  
CC inhibit the upregulation of molecules on the surface of vascular  
CC endothelial cells

**SQ** Sequence 192 AA;

**Alignment Scores:**

Pred. No.:	7e-95	Length:	192
Score:	906.00	Matches:	177
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	3	Gaps:	0

US-09-869-566-4 (1-650) x AAY95297 (1-192)

QY		106	AAGAGCTCCAAAGGTGAAGAATTAAACCGAAGAAATTCAGATTCAATGACACAGATCAC	165
Dd		22	ArgGLyProlValIleValAsnLeuasnProLysIleHisAspGlnAspHis	41
QY		166	AAAGTACTGTCTTGAGCTCTGGGAATCTCATAGCAGTTCCAGATTAAAACTACATACGC	225
Dd		42	LysValLeuValLeuaspSerLysasnLeuIleAlaValProHspLysAsnTrpIleArg	61
QY		226	CCAGAGATCTTCTTTGATTAAGCTTCATCTTAGCTCAGCTCTGCCGAGAAAAGAGT	285
Dd		62	ProGluIlePhePheIleAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLysGlySer	81
QY		286	CCGATTCTCTGGGGGCTCTTAAAGGGAGTTTTGTCTTACTGTGACAGAGATAAAGGA	345
Dd		82	ProlIleLeuLeuGlyValSerLysGlyGluPheCysLeuTrpCysAspLysAspLysGly	101
QY		346	CAAAGTCATCCATCCCTTCAGCTGAAGAAAGAGAACGATGAAGCTGGCGCCCAAAG	405
Dd		102	GlnSerHisIleProSerLeuGlnIleuLysIleGluLysLeuMetLysLeuAlaAlaGlnLys	121
QY		406	GAATCAGCAGCGCGCGCCCTTCATCTTTTAATAGGCTCAGTGGCGCTCCTCGAMACATCTG	465
Dd		122	GlnSerAlaIleArgIleProPheIleIlePheTrpAlaGlnValGlySerTrpAsnMetLeu	141
QY		466	GAGTCGGCGGCTCACCCCGAGATGTTCAATCTTGACCTCTGSCAATTTGTAATGAGCTGTT	525
Dd		142	GlnSerAlaAlaHisIleProGlyTrpPheIleIleCysThrSerCysAsnCysAsnGluProVal	161
QY		526	GGGGTACACGATTAATTTGAGAACHGAGAAACACATTTGAATTTTCATTTCAACCACTTTC	585
Dd		162	GlyValThrAspLysPheGlnAsnArgLysHisIleGluPheSerPheGlnProValCys	181
QY		586	AAAGCTGAATAGACCCCACTGAGGTCAAGCAT	618
Dd		182	LysAlaGlnMetSerProSerGluValIleSerPhe	192

### RESULT 3

ID ADN05880 standard; protein; 192 AA.

AC ADN05880 ;

DT 01-JUL-2004 (first entry)

DE Antipsoriatic protein sequence #1103.

KW antipsoriatic; gene therapy; psoriasis; diagnosis.

**Homo sapiens**

PN WO2004028479-A2.

PD 08-APR-2004.

25-SEP-2003; 2003WO-US030907.

PR 25-SEP-2002; 2002US-0414006P.

XX (GETH ) GENENTECH INC.  
PA  
PT

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
ST

[illegible]

DR N-PSDB; ADN05879.

PT New PRO nucleic acid or polypeptide, useful for preparing a

PT mammal.

CC The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polypeptides of the invention.

Sequence 192 AA;

Alignment Scores:

Pred. No.:	7e-95	Length:	152
Score:	96.00	Matches:	177
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	8	Gaps:	0

US-09-869-566-4 (1-650) x ADN05880 (1-192)

Qy	106	AAAGGCTCAAAAGTAAAGAACTTAAACCCGAAAGAAATTCAGATCTCAAGACATGAC	165
Db	22	ArgGlyProIyValIyAsnIeuAsnProIySlySPrIeSeriIeHsVsrGlnAspIeHs	41
Qy	166	AAAGTACTGGTCTGGACTCTGGGATGTCATPAGCAGTTCCAGATAAAAAATCATATCGC	225
Db	42	LysValIleuValIleuAspSerGlyAsnIeuIleuIleuAlaProAspIyAsnIyTlleArg	61
Qy	226	CCAGAGATCTTCTTTGCAATTAGCCCTCATCCCTTGAAGCTCAGCCCTCGCGAGAAAGAAAGT	285
Db	62	ProGluIleIerPheHalaIeuAlaIeSerIeIeuSerIeAlaSerIeAlaGluIyVgIySer	81
Qy	286	CCGATTTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGAACAAGATAAAGGA	345
Db	82	ProIleIeuIeuGlyValIeSerIyGlyIuPheCysIeuIyTxCysAspIyAspIyVgIy	101
Qy	346	CAAAAGTCATCATCCCTTCAGCTGAAGAAGAGAAACATGATGAAGCTGGCCGCCAAAG	405
Db	102	GlnSerHAsProIeSerIeuGlnIeuIyVgIuIyVleuIeuIyVleuAlaIaIaGlnIyS	121
Qy	406	GAATCAGACAGCCGAGCCCTTCATCTTTATAGGGCTCAGTGGGCTCTGGAAATGCTG	465
Db	122	GlnSerAlaIAsArgIyProPheIlePheIyTArgIaGlnIyAlaGlySerTrpAsnMetIeu	141
Qy	466	GAGTGCGGGCTCAGCCCGGATGGTTCATCTGACACCTCGGCATTTATAGAGCCGTT	525
Db	142	GlnSerAlaIaIaHAsProGlyTTrpPheIleCysHnIeSerCysAsnIyCysAsnGluProVal	161
Qy	526	GGGGTGACAGATAAATTTGAGAACAGAAACACATTTGATATTTTCACACAGTTTGC	585
Db	162	GlyValIleHAspIyPheGlnAsnArgIyHAsIleGlnPheSerPheGlnProValCys	181
Qy	586	AAAGCTGAATAGGCCCCAGTGAAGTTCAGCAT	618
Db	182	LysAlaGlnMetSerProSerGlnValaSerAsp	192

## RESULT 4

ID AAY95300 standard; protein; 197 AA.





CC polypeptide. The IL-1H4 polypeptide, polynucleotides and  
CC recombinant methodology. The IL-1H4 polypeptide, polynucleotides and  
CC modulators are useful for treating chronic and acute inflammation,  
CC septicemia, autoimmune diseases (e.g., inflammatory bowel disease,  
CC psoriasis and arthritis), transplant rejection, graft versus host  
CC disease, infection, stroke, ischemia, acute respiratory disease syndrome,  
CC allergies, asthma, osteoarthritis, brain injury, AIDS, bone diseases (e.g.,  
CC osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive  
CC heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4  
CC polynucleotides are useful as diagnostic reagents and for chromosome  
CC identification. The present sequence represents the IL-1H4 mature  
CC polypeptide

**SQ Sequence 198 AA;**

**Alignment Scores:**

Pred. No.:	1.3e-93	Length:	199
Score:	895.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.92%	Indels:	0
DB:	4	Gaps:	0

US-09-869-566-4 (1-650) x AAB85138 (1-198)

QY	1172	CTGGTCTCTGAGCTCTGGGAATTCATAGCAGTTCCAGATTAATAAACTACATACGCCCAAG	2311
Db	50	LeuValLeuAspSerLeuYasnLeuLleAlaValProAspLysAsnTrpLleArgProGlu	69
QY	2332	ATCTTCTTTGACATTAGCCTCATCTCTTGAGCTCAGCCTCGCGAGAAAGAAAGTCCGATT	2911
Db	70	LlePhePheAlaLeuAlaIAserSerIeuserSerAlaSerAlaGluLysGlySerProIle	89
QY	292	CTTCCTGGGGGCTCTTAAGGGGAGTTTGTCTTACTGTGAACAAGATTAAGACAAAGT	3511
Db	90	LeuLeuGluValSerLysGlyGluPheCysLeuTrpCysAspLysAspLysGlyGlnSer	1091
QY	352	CATCCATCCCTTCAGCTGMAAGAAAGAAACTGATGAAGCTGGCTGCCCAAAAGAAATCA	4111
Db	110	HisProSerLeuGlnLeuLysLysGlyLysLeuMetLysLeuAlaAlaGlnLysGlnSer	1281
QY	412	GCAAGCGGAGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTCGGAACATGCTGAGTCG	4711
Db	130	AlaArgArgProPheLlePheTrpArgAlaGlnValGlySerTrpAsnMetLeuGlnSer	1491
QY	472	GGGGCTCAGCCCGGAGTGGTTGATCTGCACTTCCTCGCATTTGATTAAGGCTGGTGGGGTG	5311
Db	150	AlaAlaAlaProGluTrpPheLleCysTrpSerCysAsnCyAsnGlnProValGlyVal	1691
QY	532	ACAGATTAATTTGAGAACGAGAAACACATTGAAATTTTCATTTCACCAAGTTGGCAAGCT	5911
Db	170	ThrAspLysPheGluAsnAspLysHisIleGluPheSerPheGlnProValCysLysAla	1891
QY	592	GAATGAGCCCAAGTGAAGGTCAGCAT	618
Db	190	GluMetSerProSerLeuValSerAsp	198

## RESULT 6

AA96938 standard; protein; 207 AA.

AC AY969387

DT 31-OCT-2000 (first entry)

Human IL-1 receptor antagonist 1 long.

hIL-1RAcL; human interleukin-1 receptor antagonist-1 long; IL-1lp;

KM	anti-aschmatic; anti-arthritis; antimicrobial; respiratory; vaccine
KW	anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
KV	gene therapy.
XX	Homo sapiens.
OS	
XX	
IN	WO200039297-A2.

OS Homo sapiens

PN WO200039297-A2

PD 06-JUL-2000.

PF 22-DEC-1999; 99WO-US030720.

PR 23-DEC-1998; 98US-0113430P.

PR 13-APR-1999; 99US-0129122P.

PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.

PI Goddard A, Pan J;

DR WPI; 2000-452395/39



PT preventing and treating e.g. inflammation, asthma and psoriasis.

PS Claim 22; Fig 15; 143pp; English.

CC An isolated nucleic acid molecule encoding an interleukin-1-like  
CC polypeptide (IL-11p) that retains one or more activities of the peptide  
CC from which it is derived, such as the IL-18R binding activity of a human  
CC interleukin-1 receptor antagonist-1 (hIL-1Ra) polypeptide, is new. The  
CC nucleic acids may be used in molecular engineering applications, e.g.  
CC hybridization assays and chromosome and gene mapping studies, for  
CC recombinantly producing the IL-11p polypeptide or for producing gene  
CC knock out animals to study the role of the protein in metabolism and  
CC disease processes (conversely, gene therapy protocols may be used to  
CC supplement a patient's production of the polypeptide or to rectify  
CC mutations that lead to the production of an active peptide). The  
CC peptides produced may be used to screen for and produce modulators (e.g.  
CC antibodies) of IL-11p protein expression and activity which may be used to  
CC treat disorders associated with inappropriate IL-11p expression and  
CC activity, such as inflammatory disorders, asthma, arthritis,  
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress  
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,  
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.

**SQ Sequence 207 AA;**

Alignment Scores:	
Pred. No.:	1.32e-93
Score:	895.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	78.92%
DB:	3
Length:	207
Matches:	169
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-869-566-4 (1-650) x AAY96938 (1-207)

QY	112	CCAAAGGGGAAGAACTTAAACCCGAAGAAATTCAGATTCATGACCGAGATTCACAAAGTA	171
Db	39	ProlysvAllyAsnIleuAsnProlyAlaPheSerIleIhIsapGlnAphIIslyVal	58
QY	172	CTGGTCTCGAGACTCTGGGAATCTCATAGCAAGTTCAGATTAACCATACATACGCCAGAG	231
Db	59	IeuValIleuAspSerGlyAsnIleuIleAlaValProAspIlyAsnIyrIleAspProGlu	78
QY	232	ATCTTCCTTGGCATTCAGCTCATTCCTTGAGCTCAGCTCTCGGAGAAAGAGATCGCATT	291
Db	79	IlePhePheIleAlaIleAlaSerSerIleuSerSerIleAsnIleGluIlySglYserProIle	98
QY	292	CTCTCGGGGGTCTCTAAAGGGAGATTTCCTCTACTGTGACAAAGATTAAGACAAAGT	351

D8	99	LeuLeuGlyValSerLysGlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSer	118
QY	352	CATCCATCCCTTTCAGCTGAAGAGAGAACTGATGAAGCTGCTGCCAAAGAAATCA	411
D8	119	HisProSerLeuGlnLeuLysLysGlnLysLeuMetLysLeuAlaGlnLysGlnSer	138
QY	412	GCACGCCGGCCCTTCATCTTTTATTAAGGGCTCAGGTGGGCTCTTGAAACATGCTGGAGTCG	471
D8	139	AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTPAamMetLeuGlnSer	158
QY	472	GGCGCTACCCCGGATGGTTATCATCTGACCCCTCCGCAATGTTATGAAGCCGTGGGGGTG	531
D8	159	AlaIleHisProGlyTyrPheIleCysHisSerCysAsnGlnProValGlyVal	178
QY	532	ACAGATAAATTGGAACACAGAAACACATTGAATTTTCATTTCAACAGATTGCAAGCT	591
D8	179	ThrAspLysPheGluAsnArgLysHisIleGluPheSerPheGlnProValCysLysAla	198
QY	592	GAAATGAGCCCCAGTGAAGCTACGCAT	618
D8	199	GluMetSerProSerGluValSerAsp	207
RESULT 7			
AA70927	ID	AA70927 standard; protein, 218 AA.	
XX	XX	AA70927;	
AC	AC		
DT	DT	05-SEP-2000 (first entry)	
DE	DE		
DE	DE	Human zllia4 protein.	
XX	XX		
KW	KW	Human interleukin-1, IL-1; zllia4 protein; inflammation; arthritis;	
KW	KW	psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;	
KW	KW	anaemia; inflammatory bowel disease; acute neuropathology; shock;	
KW	KW	chronic neuropathology; respiratory disease syndrome; restenosis;	
KW	KW	acquired immune deficiency syndrome; AIDS; anti-inflammatory; cytostatic;	
KW	KW	anti-arthritic; anti-psoriatic; antibacterial; immunosuppressive;	
KW	KW	anti-anaemic; neuroprotective; vasotropic;	
XX	XX	anti-human immunodeficiency virus; HIV.	
OS	OS	Homo sapiens.	
XX	XX		
Key	Key	Location/Qualifiers	
Domain	Domain	60..64	
FT	FT	/label= Beta_strand	
FT	FT	65..67	
FT	FT	/note= "Variable loop region involved in receptor binding"	
FT	FT	68..72	
FT	FT	/label= Beta_strand	
FT	FT	73..76	
FT	FT	/note= "Variable loop region involved in receptor binding"	
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FT	FT	/label= Beta_strand	
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FT	FT	/note= "Variable loop region involved in receptor binding"	
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FT	/note="Variable loop region involved in receptor binding"	
FT	Domain	187..189
FT	/label= Beta_strand	
FT	Domain	190..200
FT	/note="Variable loop region involved in receptor binding"	
FT	Domain	201..204
FT	/label= Beta_strand	
XX		
PN	WO20024699-A2.	
PD	04-MAY-2000.	
XX		
PF	27-OCT-1999;	99WO-US025038.
XX		
PR	27-OCT-1998;	98US-00179614.
XX		
PA	(ZTMO ) ZYMOGENETICS INC.	
PI	West RR, Shepard PO, Gao Z;	
DR	WPI; 2000-350740/30.	
XX	N-PSTDB: AAD00210.	
PT	Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host disease, leukemia.	
PS	Claim 4; Fig 2; 8pp; English.	
CC	The present sequence is the human interleukin (IL)-1 homolog zilla4 protein. This protein contains a core structure of 12 beta-strands wound into a beta-barrel, with the beta-strands separated from each other by loops. The loops between these beta-strands are highly variable among the family members and are believed to be involved in receptor binding. The zilla4 proteins modulate inflammation and other immunological processes and are therefore useful for treatment of arthritis, psoriasis, septic shock, graft-versus-host disease and leukaemia. Other diseases that may be modulated by zilla4 proteins include cancer, anaemia, inflammatory bowel disease, acute and chronic neuropathologies, shock, respiratory disease syndrome, restenosis and acquired immune deficiency syndrome	
SQ	Sequence 218 AA;	
Alignment Scores:		
Pred. No.:	1.34e-93	Length: 218
Score:	895.00	Matches: 169
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	78.92%	Indels: 0
DB:	3	Gaps: 0

```

QY 112 CCAAGGTGAAGACTTTAAACCCGAAGAAATTGACGATTCATGACCAGATCAAAAGTA 171
Db 50 ProllyVallyAsnLeuEnuEnProllySlyPheSerIleHisAspGlnAspHislyVal 69
QY 172 CTGGTCTTGAGACTCTGGGAATCTCATAGCAAGTTCCAGATTAATAATACATACGCCAGAG 231
Db 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspIlyAsnIlyrIleArgProGlu 89
QY 232 ATCTTTCTTGATTAAGCTTCATCTTGAGCTCAGCTCTCCGGAAGAAAGAAATCCGATT 291
Db 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIleAlaGlnlySgllySerProIle 109
QY 292 CTCCTGGGGGCTCTTAAAGGGAGGAGTTTGTCTTACCTGAGCAAGGATAAGAGCAAAAGT 351
Db 110 LeuLeuGlyValSerlySgllyGluPheCysLeuIlyrCysAspIlyAspIlySgllyIns 129
QY 352 CATTCATCTCCCTTGAGCTGAAGAGAGAACTGATGAAGCTGAGCTGCCCAAGAAATCA 411
Db 130 HisProSerLeuEnuEnuIlySlySgllyLeuMetlyLeuAlaIleGlnlySgllyIns 149
QY 412 GCACGCCGGGCTCTTCAATCTTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGAGTGG 471
Db 150 AlaArgArgProPheIlePheIlyrArgAlaGlnValGlySerTrpAsnMetLeuGlnSer 169
QY 472 GCGGGCTCACCCCGGATGGTTTCATCTGCACTCTGCAATTGATAGAGCTGTGGGGTG 531
Db 170 AlaAlaHisProGlyTrpPheIleCysTrpSerCysAsnIlyAsnGlnProValGlyVal 189
QY 532 ACAGATAAATTTGAGAACAGAAACAAATTTGATTTTCAACCAAGTTTCAAAAGCT 591
Db 190 ThrAspIlyPheGluAsnIlySlyHisIleGlnPheSerPheGlnProValCyslySAla 209
QY 592 GAAATGAGCCCCAGTAGAGTACCGAT 618
Db 210 GluMetSerProSerGlyValSerAsp 218

RESULT 8
ID AAY91885 standard; protein; 218 AA.
AC AAY91885;
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Primate interleukin-1 like molecule (IL-1-zeta) alternative sequence.
XX
XX Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;
XX hypoglycemia; plasma iron; plasma zinc; acute liver response;
XX plasma copper.
XX
XX Mammalia.
OS
XX
XX Key Location/Qualifiers
FH 58..64 /label= beta_strand_1
FT /label= beta_strand_1
FT 69..74 /label= beta_strand_2
FT /label= beta_strand_2
FT 76..80 /label= beta_strand_3
FT /label= beta_strand_3
FT 91..96 /label= beta_strand_4
FT /label= beta_strand_4
FT 100..106 /note= "forms a loop which is part of a primary binding
FT /note= "forms a loop which is part of a primary binding
FT 107..113 segment to the IL-1 receptor type"
FT /label= beta_strand_5
FT /label= beta_strand_5
FT 118..126 /label= beta_strand_6
FT /label= beta_strand_6
FT 131..136 /label= beta_strand_7
FT /label= beta_strand_7
FT 154..161 /label= beta_strand_8
FT /label= beta_strand_8

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FT Domain 163..169
FT /label= beta_strand_9
FT 176..180 /label= beta_strand_10
FT /label= beta_strand_10
FT Domain 185..204
FT /label= beta_strand_11
FT /label= beta_strand_11
FT Domain 201..204
FT /label= beta_strand_12
XX
XX MO200017363-A2.
XX
XX 30-MAR-2000.
PD
XX
XX 17-SEP-1999; 99WO-US020868.
PF
XX
XX 18-SEP-1998; 98US-00156966.
PR
XX
XX (SCHER) SCHERING CORP.
PA
XX
XX Timans JC;
PI
XX
XX MPI; 2000-283588/24.
DR
XX
XX N-PSDB; AAA08513.
PT
XX
XX New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
PT for diagnostic and therapeutic purposes, comprises a 128 amino acid
PT sequence.
XX
XX Claim 1; Page 103-104; 110pp; English.
PS
XX
XX The present sequence is an alternative primate interleukin-1 like
CC molecule, designated IL-1-zeta. The 12 beta strands, indicated in the
CC features table, fold into a beta-trefoil fold. The specification claims
CC an isolated or recombinant polypeptide that: (a) specifically binds
CC polyclonal antibodies generated against at least a 12 consecutive amino
CC acid segment of IL-1-zeta (see AAY91884) or its allelic variant (see
CC AAY91885); and (b) comprises at least one sequence selected from:
CC AAY91886-903 or AAY91904-06. The preferred 12 consecutive amino acid
CC segment is chosen from AAY91907-18 or AAY91919-21. IL-1-zeta is likely to
CC play a role in systemic inflammatory reactions, such as fever,
CC hypoglycemia, reduced plasma iron and zinc, the acute response of the
CC liver, and increase plasma copper. IL-1-zeta binding compounds
CC (comprising antigen binding sites) and IL-1-zeta polypeptides are also
CC useful for both diagnostic and therapeutic purposes
XX
XX
XX Sequence 218 AA;
SQ
XX
XX Alignment Scores:
XX Pred. No.: 1,34e-93 Length: 218
XX Score: 895.00 Matches: 169
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 78.92% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-869-566-4 (1-650) x AAY91885 (1-218)
QY 112 CCAAGGTGAAGACTTTAAACCCGAAGAAATTGACGATTCATGACCAGATCAAAAGTA 171
Db 50 ProllyVallyAsnLeuEnuEnProllySlyPheSerIleHisAspGlnAspHislyVal 69
QY 172 CTGGTCTTGAGACTCTGGGAATCTCATAGCAAGTTCCAGATTAATAATACATACGCCAGAG 231
Db 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspIlyAsnIlyrIleArgProGlu 89
QY 232 ATCTTTCTTGATTAAGCTTCATCTTGAGCTCAGCTCTCCGGAAGAAAGAAATCCGATT 291
Db 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIleAlaGlnlySgllySerProIle 109
QY 292 CTCCTGGGGGCTCTTAAAGGGAGGAGTTTGTCTTACCTGAGCAAGGATAAGAGCAAAAGT 351
Db 110 LeuLeuGlyValSerlySgllyGluPheCysLeuIlyrCysAspIlyAspIlySgllyIns 129

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QY 352 CATCATCCCTTCACTGAAAGAGAGAACTGATGAAGCTGCTGCCCAAAAGAAATCA 411
DB 130 HIsProSerLeuIndLeuylsYsGIuYsLeuMetLysLeuAlaIaGIuYsGIuSer 149
QY 412 GCACGCCGGCCCTCAATCTTTATAGGGCTCAGGTGGCTCCCGAAACATGCTGAGGTG 471
DB 150 AAlaArgProPheIlePheYrArgAlaGlnValGlySerThrPasnMetLeuGIuSer 169
QY 472 GCGGCTCACCCCGAGATGTTCACTGACACCTCCTGCATTTGTAATGAGCTGTGGGGTG 531
DB 170 AAlaIleHisProGlyTrpPheIleCysThrSerCysAsnGlySerGlnuProValGlyVal 189
QY 532 ACAGATAAATTTGAGAACACAGAAACATTTGATTTTCATTTCACACGTTTGCAAGCT 591
DB 190 ThrAspLysPheGluAsnArgLysHisIleGluPheSerPheGlnProValCysLysAla 209
QY 592 GAAATGAGCCCGCATGAGTCAAGCAT 618
DB 210 GluMetSerProSerGluValSerAsp 218

RESULT 9
AA95299
ID AAY95299 standard; protein; 218 AA.
AC AAY95299;
DT 12-SEP-2000 (first entry)
XX
DE Human interleukin-1 zeta splice variant TDZ.1.
XX
KW Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.1;
KW testis-derived zeta variant; therapy; inflammation; fever.
OS Homo sapiens.
XX
PN WO200036108-A2.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99MO-US029549.
PR 14-DEC-1998; 98US-0112163P.
PR 10-NOV-1999; 99US-0164675P.
XX
PA (IMMV ) IMMUNEX CORP.
PI Sims JE, Smith DE, Born TL;
XX
DR MPI; 2000-442387/38.
DR N-PSDB; AAA27920.
XX
PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and insulin-
PT dependent diabetes mellitus.
XX
PS Claim 10; Page 11; 87pp; English.
XX
XX The present sequence is that of splice variant TDZ.1 (testis-derived zeta
XX variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA is generated
XX from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and the encoded
XX protein is probably a functional IL-1 like molecule. TDZ.1 mRNA is
XX expressed most strongly in the kidney, skeletal muscle, testis, prostate,
XX ovary, colon, small intestine, liver, placenta, lung, tonsil, foetal
XX liver, lymph node and bone marrow. The invention is directed to novel,
XX purified and isolated IL-1 zeta, its splice variants and Xrec2
XX polypeptides (see AAY95297-301), the nucleic acids (see AAA27918-22)
XX encoding such polypeptides, processes for production of recombinant forms
XX of such polypeptides, and their uses. The polypeptides can be used to
XX study cellular processes such as immune regulation, cell proliferation,
XX cell death, cell migration, cell-to-cell interaction and inflammatory
XX responses, to identify proteins associated with IL-1 zeta, to screen for
XX potential inhibitors, and to prepare antibodies. In particular, they can

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CC be used to activate and/or inhibit the activation of vascular endothelial
CC cells and lymphocytes, induce and/or inhibit the induction of local
CC tissue destruction and fever, inhibit and/or stimulate macrophages and
CC vascular endothelial cells to produce IL-6, induce and/or inhibit the
CC induction of proestrogens, nitric oxide synthetase, and
CC metalloproteases, and upregulate and/or inhibit the upregulation of
CC molecules on the surface of vascular endothelial cells
XX
SQ Sequence 218 AA;
Alignment Scores:
Pred. No.: 1,34e-93 Length: 218
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: Gaps: 3
US-09-869-566-4 (1-650) x AAY95299 (1-218)
QY 112 CCAAGGTGAAAGAACTTAAACCCGAAAGAAATTCAAGATTCAGACAGATCAAGATCA 171
DB 50 ProLysValLysAsnLeuAsnProLysLysPheSerIleHisAspGlnAspHisLysVal 69
QY 172 CTGCTCTGAGCTCTGGGAATCTCATPAGCATGTTCCAGATTAATACTTACATACGCCAGAG 231
DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTrpIleArgProGlu 89
QY 232 ATCTTCTTGATTTAGCCCTTCATCCCTTGAGCTTCAGCTCTCGCGAAGAAAGAAAGTCCGAT 291
DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLysGlySerProIle 109
QY 292 CTCCTGGGGGCTCTTAAAGGGAGATTGTCCTCTACTGTCAGCAAGATTAAGACAAAGT 351
DB 110 LeuLeuGlyValSerLysGlyLysPheCysLeuTrpCysAspLysAspLysGlyLysLeu 129
QY 352 CATCATCCCTTCACTGAAAGAGAGAACTGATGAAGCTGCTGCCCAAAAGAAATCA 411
DB 130 HIsProSerLeuIndLeuylsYsGIuYsLeuMetLysLeuAlaIaGIuYsGIuSer 149
QY 412 GCACGCCGGCCCTTCAATCTTTATAGGGCTCAGGTGGCTCCCGAAACATGCTGAGGTG 471
DB 150 AAlaArgProPheIlePheYrArgAlaGlnValGlySerThrPasnMetLeuGIuSer 169
QY 472 GCGGCTCACCCCGAGATGTTCACTGACACCTCCTGCATTTGTAATGAGCTGTGGGGTG 531
DB 170 AAlaIleHisProGlyTrpPheIleCysThrSerCysAsnGlySerGlnuProValGlyVal 189
QY 532 ACAGATAAATTTGAGAACACAGAAACATTTGATTTTCATTTCACACGTTTGCAAGCT 591
DB 190 ThrAspLysPheGluAsnArgLysHisIleGluPheSerPheGlnProValCysLysAla 209
QY 592 GAAATGAGCCCGCATGAGTCAAGCAT 618
DB 210 GluMetSerProSerGluValSerAsp 218

RESULT 10
AA96940
ID AAY96940 standard; protein; 218 AA.
AC AAY96940;
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1 receptor antagonist 1 V.
XX
KW hIL-1RA1V; human interleukin-1 receptor antagonist-1; IL-1IP;
KW osteopontin; interleukin-1-like polypeptide; anti-inflammatory;
KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
XX gene therapy.
OS Homo sapiens.

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XX MO200039297-A2.  
 PN 06-JUL-2000.  
 XX 22-DEC-1999; 99WO-US030720.  
 XX 23-DEC-1998; 98US-0113430P.  
 PR 22-JAN-1999; 99US-0116843P.  
 PR 13-APR-1999; 99US-0129122P.  
 XX (GETH ) GENENTECH INC.  
 PA  
 PI Goddard A, Pan J;  
 XX WPI; 2000-452395/39.  
 DR N-PSDB; AAA51604.  
 XX  
 PT Nucleic acids encoding interleukin-1-like polypeptides, useful for  
 PT preventing and treating e.g. inflammation, asthma and psoriasis.  
 XX  
 PS Claim 22; Fig 19; 143pp; English.  
 XX  
 XX An isolated nucleic acid molecule encoding an interleukin-1-like  
 CC polypeptide (IL-11p) that retains one or more activities of the peptide  
 CC from which it is derived, such as the IL-18R binding activity of a human  
 CC interleukin-1 receptor antagonist-1 (IL-1Ra) polypeptide, is new. The  
 CC nucleic acids may be used in molecular engineering applications, e.g.  
 CC hybridization assays and chromosome and gene mapping studies, for  
 CC recombinantly producing the IL-11p polypeptide or for producing gene  
 CC knock out animals to study the role of the protein in metabolism and  
 CC disease processes (conversely, gene therapy protocols may be used to  
 CC supplement a patient's production of the polypeptide or to rectify  
 CC mutations that lead to the production of an active peptide). The  
 CC peptides produced may be used to screen for and produce modulators (e.g.  
 CC antibodies) of IL-11p protein expression and activity which may be used to  
 CC treat disorders associated with inappropriate IL-11p expression and  
 CC activity, such as inflammatory disorders, asthma, arthritis,  
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress  
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,  
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease  
 XX  
 XX Sequence 218 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.34e-93 Length: 218  
 Score: 895.00 Matches: 169  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 78.92% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-869-566-4 (1-650) x AAY96940 (1-218)  
 QY 112 CCAAGGTGAGAACTTAAACCCGAGAATTGAGATTCAGACGAGATCAAGTA 171  
 DB 50 ProllyVallyahennunproulyslvpheserillehshpshlshpshlshlval 69  
 QY 172 CTGGTCTGAGACTCTGGAAATCTCATGAGAGTTCCAGATAAAACTACATACGCCGAG 231  
 DB 70 LeuValIleuAspserGlyhennuilelaIvalProAspIysenrrylleatgProGlu 89  
 QY 232 ATCTTTTGGCATTTAGCCATCTTCATGAGCTCAGCTTCGCGAGAAAGAGATCCGATT 291  
 DB 90 IlePhePheAlaIleuAlaSerSerIleuSerSerAlaSerIaGluIuysGlySerProIle 109  
 QY 292 CTGCTGGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTCGACAAAGGTAAGGCAAGT 351  
 DB 110 LeuIleuGlyValserIygluIupheCyIleuTyCyahpIyAspIyAspIygluIuSer 129  
 QY 352 CATTCATCCCTTCAGCTGAAGAGAAAGAGAACTGATGAAGCTGGCTCCCAAAAGATCA 411  
 DB 130 HisProSerIleuGlnIleuIyIygluIuIyIleuMetIyIleuAlaIaGlnIyIygluIuSer 149

QY 412 GCACGCCGCGCTTCATCTTTTATAGAGGCTCAGTGGGCTCCTGGAACATGCTGAGTGC 471  
 DB 150 AlaIArgArgProPheIlePheIleTyArgAlaGlnIvalGlySerTrpAsnMetIeuGluSer 169  
 QY 472 GCGGCTCACCCCGAGTGTTCATCTGCACCTCTGCAATTTGATAGAGCTGTGGGGTG 531  
 DB 170 AlaAlaIleProGlyTrpPheIleCysThrSerCysAsnCyAsnGluProValGlyVal 189  
 QY 532 ACAGATTAATTTGAGAACAGGAAACACATTTGATTTTCATTCACACGATTTGCAAGCT 591  
 DB 190 ThrAspIyPheGluAsnArgIyShIstIleGluPheSerPheGlnProValCyIyAsAla 209  
 QY 592 GAAATGAGCCCGAGTGGAGTCCGAT 618  
 DB 210 GluMetSerProSerGluValSerAsp 218  
 RESULT 11  
 AAB28266  
 ID AAB28266 standard; protein; 218 AA.  
 XX  
 AC AAB28266;  
 XX  
 DT 13-FEB-2001 (first entry)  
 XX  
 DE Human Interleukin-1 homologue IL-1H4.  
 XX  
 XX Human; interleukin-1 homologue; IL-1H4; inflammation; septicemia;  
 KW autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;  
 KW transplant rejection; graft versus host disease; infection; stroke;  
 KW ischemia; acute respiratory disease; allergy; asthma; restenosis;  
 KW brain injury; AIDS; bone disease; osteoporosis; cancer;  
 KW congestive heart failure; atherosclerosis; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200063226-A1.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 14-APR-2000; 2000WO-US010207.  
 XX  
 PR 16-APR-1999; 99US-00293625.  
 XX  
 PA (SMIT ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Young PR, McDonnell PJ;  
 XX  
 DR WPI; 2000-687155/67.  
 DR N-PSDB; AAC66727.  
 XX  
 XX Interleukin-1 homolog useful for treating conditions such as chronic and  
 PT acute inflammation, septicemia, autoimmune diseases ischemia, acute  
 PT respiratory disease, allergies, and asthma.  
 XX  
 PS Claim 1; Page 28-29; 30pp; English.  
 XX  
 XX The present sequence is human interleukin-1 homologue (IL-1H4). IL-1H4 is  
 CC useful for treating conditions such as chronic and acute inflammation,  
 CC septicemia, autoimmune diseases (e.g. inflammatory bowel disease,  
 CC psoriasis, and arthritis), transplant rejection, graft versus host  
 CC disease, infection, stroke, ischemia, acute respiratory disease,  
 CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.  
 CC osteoporosis), cancer, congestive heart failure, atherosclerosis, and  
 CC Alzheimer's disease, related to either an excess of, or an under-  
 CC expression of, IL-1H4 polypeptide activity  
 XX  
 SQ Sequence 218 AA;  
 Alignment Scores:  
 Pred. No.: 1.34e-93 Length: 218  
 Score: 895.00 Matches: 169  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 78.92% Indels: 0  
 DB: 3 Gaps: 0

US-09-869-566-4 (1-650) x AAB28266 (1-218)

QY 112 CCNAAAGTGAAGAACTTAAACCCGAAAGAAATTGAGATTTCATGACCGAGATCAAAAGTA 171  
 |||||  
 DB 50 ProlysValIysAsnLeuAsnProIysLysPheSerIleHisAspGlnsPhisIysVal 69  
 |||||  
 QY 172 CTGGCTCTGAGCTCTGGGAAATCTCATAGCAGTTCCAGATAAACATACATAGCCGAGG 231  
 |||||  
 DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrIleArgProGlu 89  
 |||||  
 QY 232 ATCTCTTTGATTAAGCTCATCTTGAAGTCAAGCTCTGCGGAAAGAAATCCGATT 291  
 |||||  
 DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGlnLysGlySerProIle 109  
 |||||  
 QY 292 CTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTTACTGTGACAGGATTAAGGACAAAGT 351  
 |||||  
 DB 110 LeuLeuGlyValSerLysGlyGlnPheCysLeuTyrCysAspLysAspLysGlyGlnSer 129  
 |||||  
 QY 352 CATTCATCCCTTCAGCTGAAGAAAGAAAGAACTGATGAAGCTGGCTGCCAAAGAAATGA 411  
 |||||  
 DB 130 HisProSerLeuGlnLeuLysGlyLysLeuMetLysLeuAlaAlaGlnLysGlySer 149  
 |||||  
 QY 412 GCACGCCGCGCTTCATCTTTATAGAGGCTCAGGTGGGCTCTGGAACAATGCTGAGTGC 471  
 |||||  
 DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTrpAsnMetLeuGlnSer 169  
 |||||  
 QY 472 GCGGCTCACCCCGATGGTTTCATCTGCACTCTGCAATTGATAGAGCTGTGGGGTG 531  
 |||||  
 DB 170 AlaAlaHisProGlyTyrPheIleCysThrSerCysAsnGlnProValGlyVal 189  
 |||||  
 QY 532 ACAGATAAATTGAGAACAAGAAACATGATTTTCATTCAACAGTTGGCAAGGT 591  
 |||||  
 DB 190 ThrAspLysPheGlnAsnArgLysHisIleGlnPheSerPheGlnProValCysLysAla 209  
 |||||  
 QY 592 GAAATGAGCCCGCATGAGTCAAGCGAT 618  
 |||||  
 DB 210 GluMetSerProSerGlnValSerAsp 218  
 |||||

RESULT 12  
 AAB47186  
 ID AAB47186 standard; protein; 218 AA.  
 AC AAB47186;  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE IL-1 related polypeptide.  
 XX  
 KW Interleukin-1-related polypeptide; HPB-MLT cell; T-cell; inhibition;  
 natural killer activity; immune system; gene therapy; immunodeficiency.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1092773-A2.  
 XX  
 PD 18-APR-2001.  
 XX  
 PF 11-OCT-2000; 2000EP-00308948.  
 XX  
 PR 15-OCT-1999; 99JP-00294493.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 PI Ushio S, Nukada Y, Yamamoto K, Kurimoto M;  
 XX  
 DR WPI; 2001-275206/29.  
 XX  
 DR N-PSDB; AAC85860.  
 XX  
 PT New human interleukin-1-related polypeptide and polynucleotide, useful

PT for gene therapy and in developing drugs as regulators of natural killer  
 activity, are capable of inhibiting natural killer activity.  
 XX  
 PS Claim 1; Page 12; 15pp; English.  
 XX

CC This sequence represents an interleukin-1 (IL-1)-related polypeptide. IL-  
 CC 1 related polypeptide was isolated from HPB-MLT cells, FERM-BP-2430, an  
 CC established human T-cell line. IL-1 related polypeptide is useful for  
 CC inhibiting natural killer (NK) activity, which is related to the immune  
 CC system of mammals. The DNA encoding the IL-1 related polypeptide is  
 CC useful in gene therapy of patients in need of NK activity inhibition and  
 CC others suffering from immunodeficiency

XX  
 SQ Sequence 218 AA;  
 |||||

Alignment Scores:  
 Pred. No.: 1,34e-93 Length: 218  
 Score: 895.00 Matches: 169  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 78.92% Indels: 0  
 DB: 4 Gaps: 0

US-09-869-566-4 (1-650) x AAB47186 (1-218)

QY 112 CCNAAAGTGAAGAACTTAAACCCGAAAGAAATTGAGATTTCATGACCGAGATCAAAAGTA 171  
 |||||  
 DB 50 ProlysValIysAsnLeuAsnProIysLysPheSerIleHisAspGlnsPhisIysVal 69  
 |||||  
 QY 172 CTGGCTCTGAGCTCTGGGAAATCTCATAGCAGTTCCAGATAAACATACATAGCCGAGG 231  
 |||||  
 DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrIleArgProGlu 89  
 |||||  
 QY 232 ATCTCTTTGATTAAGCTCATCTTGAAGTCAAGCTCTGCGGAAAGAAATCCGATT 291  
 |||||  
 DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGlnLysGlySerProIle 109  
 |||||  
 QY 292 CTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTTACTGTGACAGGATTAAGGACAAAGT 351  
 |||||  
 DB 110 LeuLeuGlyValSerLysGlyGlnPheCysLeuTyrCysAspLysAspLysGlyGlnSer 129  
 |||||  
 QY 352 CATTCATCCCTTCAGCTGAAGAAAGAAACATGATTTTCATTCAACAGTTGGCAAGGT 411  
 |||||  
 DB 130 HisProSerLeuGlnLeuLysGlyLysLeuMetLysLeuAlaAlaGlnLysGlySer 149  
 |||||  
 QY 412 GCACGCCGCGCTTCATCTTTATAGAGGCTCAGGTGGGCTCTGGAACAATGCTGAGTGC 471  
 |||||  
 DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTrpAsnMetLeuGlnSer 169  
 |||||  
 QY 472 GCGGCTCACCCCGATGGTTTCATCTGCACTCTGCAATTGATAGAGCTGTGGGGTG 531  
 |||||  
 DB 170 AlaAlaHisProGlyTyrPheIleCysThrSerCysAsnGlnProValGlyVal 189  
 |||||  
 QY 532 ACAGATAAATTGAGAACAAGAAACATGATTTTCATTCAACAGTTGGCAAGGT 591  
 |||||  
 DB 190 ThrAspLysPheGlnAsnArgLysHisIleGlnPheSerPheGlnProValCysLysAla 209  
 |||||  
 QY 592 GAAATGAGCCCGCATGAGTCAAGCGAT 618  
 |||||  
 DB 210 GluMetSerProSerGlnValSerAsp 218  
 |||||

RESULT 13  
 AAG68116  
 ID AAG68116 standard; protein; 218 AA.  
 AC AAG68116;  
 DT 22-JAN-2002 (first entry)  
 XX  
 DE Human interleukin 1 family protein SEQ ID NO:2.  
 XX  
 KW Human; interleukin 1; IL-1; growth factor; Tango-77; diagnosis;  
 identification.

XX Homo sapiens.  
XX  
XX JP2001231578-A.  
XX  
XX 28-AUG-2001.  
XX  
XX 07-DEC-2000; 2000JP-00372864.  
XX  
XX 09-DEC-1999; 99JP-00349780.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX WPI; 2001-60968/70.  
XX  
XX N-PSDB; AA171179.  
XX  
XX An IL-1 family protein, used for the development of diagnostic and  
XX treatment agents.  
XX  
XX Claim 1; Page 30; 38pp; Japanese.  
XX  
XX The present sequence represents a human interleukin 1 (IL-1) family  
XX protein having a combining affinity to a receptor of a protein of human  
XX IL-1 family higher than Tango-77. The protein is useful for the  
XX development of diagnostic, treating and/or preventive agents for various  
XX diseases  
XX  
SQ Sequence 218 AA:  
  
Alignment Scores:  
Pred. No.: 1.34e-93 Length: 218  
Score: 895.00 Matches: 169  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 78.92% Indels: 0  
DB: 4 Gaps: 0  
  
US-09-869-566-4 (1-650) x AAG68116 (1-218)  
  
QY 112 CCAAGGTGAAGAACTTAAACCCGAGAAATTGACATTCATGACGATCAACAAAGTA 171  
DB 50 ProlValIlyAsnLeuAsnProLysPheSerIleHisAspGlnAspHisLysVal 69  
QY 172 CTGGTCTGAGCTCTGGAGATCTCATGACGATCCGATTAACATCAACGCGCAGAG 231  
DB 70 LeuValLeuAspSerLysLeuIleAlaValProAspLysAsnTyrIleArgProGlu 89  
QY 232 ATCTTCTTGATTAACCTCATCTGAGCTGAGCTGCGGAGAAAGAAAGTCCGATT 291  
DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGlnLysGlySerProIle 109  
QY 292 CTCTCTGGGGGTCTCTAAAGGGAGATTGTCTCTACTGTGACAAAGATAAGACAAAT 351  
DB 110 LeuLeuGlyValSerLysGlyGlnPheCysLeuTyrCysAspLysAspLysGlyGlnSer 129  
QY 352 CATTCATCCCTTCAGCTGAAGAGAAAGAACTGATGAAGTGGCTGCCCAAAAGAAATCA 411  
DB 130 HisProSerLeuGlnLeuLysLysGlnLysLeuMetLysLeuAlaGlnLysGlnSer 149  
QY 412 GCAAGCGCGGCTCTGATCTTTTATAGGGCTCAGAGTGGGCTCTGGAACAATGCTGAGTGG 471  
DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTyrPheMetLeuGlnSer 169  
QY 472 GCGGCTACCCCGGATGGTTCATCTGACCTCTCGCAATTGATAGAGCTGTGGGGTG 531  
DB 170 AlaAlaHisProGlyTyrPheIleCysTyrSerCysAsnLysAsnGlnProValGlyVal 189  
QY 532 ACGATTAATTTTGAAGACGAAACATGATGATTTTCAATTAACGATTTGCAAGCT 591  
DB 190 ThrAspLysPheGlnLysAsnArgLysHisLysGlnPheSerPheGlnProValCysLysAla 209  
QY 592 GAAATGAGCCCGAGTGGATCGATG 618  
|||||

DB 210 GluMetSerProSerGlnValSerAsp 218  
RESULT 14  
AAB85136  
ID AAB85136 standard; protein; 218 AA.  
XX  
XX AAB85136;  
AC  
XX 22-AUG-2001 (first entry)  
DT  
XX  
XX Interleukin-1 homologue (IL-1H4) polypeptide.  
DE  
XX  
XX Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;  
XX immunosuppressive; antipruritic; antiarthritic; cytostatic; antiHIV;  
XX cerebroprotective; antiaesthetic; vasotropic; vulnary; osteopathic;  
XX immunostimulant; antiatherosclerotic; nootropic; neuroprotective;  
XX gene therapy; vaccine.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..20  
FT /note= "signal peptide"  
FT Cleavage-site 20..21  
FT Protein 21..218  
FT /note= "specifically claimed mature protein (AAB85138)"  
XX  
XX WO200140247-A1.  
XX  
XX 07-JUN-2001.  
XX  
XX 30-NOV-2000; 2000WO-US032521.  
XX  
XX 01-DEC-1999; 99US-00452140.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX Kumar S, McDonnell PC, Young PR;  
XX WPI; 2001-389949/41.  
XX N-PSDB; AAF84120.  
XX  
XX Novel Interleukin-1 homolog, IL-1H4, for treating chronic and acute  
XX inflammation, septicemia, autoimmune diseases, transplant rejection,  
XX graft versus host disease, stroke, ischemia, allergy and asthma.  
XX  
XX Example; Page 29; 30pp; English.  
XX  
XX The invention provides an isolated interleukin-1 homologue, IL-1H4  
XX polypeptide. The IL-1H4 polypeptide can be expressed by standard  
XX recombinant methodology. The IL-1H4 polypeptide, polynucleotides and  
XX modulators are useful for treating chronic and acute inflammation,  
XX septicemia, autoimmune diseases (e.g., inflammatory bowel disease,  
XX psoriasis and arthritis), transplant rejection, graft versus host  
XX disease, infection, stroke, ischemia, acute respiratory disease syndrome,  
XX allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,  
XX osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive  
XX heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4  
XX polynucleotides are useful as diagnostic reagents and for chromosome  
XX identification. The present sequence represents the IL-1H4 polypeptide  
XX  
SQ Sequence 218 AA:  
  
Alignment Scores:  
Pred. No.: 1.34e-93 Length: 218  
Score: 895.00 Matches: 169  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 78.92% Indels: 0  
DB: 4 Gaps: 0  
  
US-09-869-566-4 (1-650) x AAB85136 (1-218)

QY 112 CCAAGGTGAAGACTTAAACCGAAGAAATTGAGATTGATGACCAAGATCAAAAGTA 171  
DB 50 ProlysValIysAsnLeuAsnProIysPheSerIleHisAspGlnAspHisIysVal 69  
QY 172 CTGGTCTCTGAGCTCTGGAGATCTCATAGAGAGTTCCAGATAAACATACAGCCAGAG 231  
DB 70 LeuValIeuAspSerIleuAsnLeuIleAlaValProAspIysAsnIleAlaGProGlu 89  
QY 232 ATCTTCTTTGCAATTAGCTTCATCTTGAAGCTGAGCTGCGGAGAAAGAGTCCGATT 291  
DB 90 IlePhePheAlaIleuAlaSerSerIleuSerSerIleAlaGluIysGlySerProIle 109  
QY 292 CTCCTGGGGGTCTCTTAAAGGGAGTTTGTCTTACTGACAGCAAGATTAAGACAAGT 351  
DB 110 LeuLeuGlyValSerIysGlyIuPheCysLeuIlyrCysAspIysAspIysGlyIuSer 129  
QY 352 CATCCATCCCTTACGTGAAGAAAGAGAACTGATGAGCTGGCCCAAAAGAAATCA 411  
DB 130 HisProSerLeuIleuIlySlySlyIySleuMetIysLeuAlaIleGlnIySlyIuSer 149  
QY 412 GCACGCCGCCCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACAATGCTGAGTGC 471  
DB 150 AlaArgArgProPheIlePheIlePheIleArgAlaGlnValGlySerIlePheMetIeuGlyIuSer 169  
QY 472 GCGGCTACCCCGAGATGTTCACTGACCTCTGCAATTGATAGAGCTGTGGGGTG 531  
DB 170 AlaAlaHisProGlyIlePheIleCysIleHisSerCysAsnGlyAsnGluProValGlyVal 189  
QY 532 ACAGATAATTTGAGAACAGGAACACATTTTCATTTCAACAGATTTGCAAAAGT 591  
DB 190 ThrAspIysPheGluAsnArgIySlyHisIleGluIyPheSerPheGlnProValCysIySlyAla 209  
QY 592 GAAATGAGCCCCAGTGAAGTCAAGCGAT 618  
DB 210 GluMetSerProSerGluValSerAsp 218

RESULT 15  
ADJ88306  
ID ADJ88306 standard; protein; 218 AA.  
XX

ADJ88306;

06-MAY-2004 (first entry)

Human interleukin-1zeta protein variant.

Interleukin-1zeta; gene therapy; immune system; haematopoietic cell;

inflammatory disorder; infection; allergy; cancer; human.

Homo sapiens.

Location/Qualifiers

30..41 "Epitope"

45..50 "Epitope"

46..60 "Epitope"

107..113 "Epitope"

156..167 "Epitope"

163..169 "Epitope"

163..169 "Epitope"

163..169 "Epitope"

163..169 "Epitope"

163..169 "Epitope"

PA (SCHE ) SCHERING CORP.  
XX  
PI Timans JC;  
XX  
DR WPI: 2004-189656/18.  
DR N-PSDB; ADJ88305.  
XX  
PT New nucleic acid molecules encoding mammalian interleukin-1 polypeptides,  
PT useful for diagnosing, preventing or treating diseases associated with  
PT abnormal expression of interleukin, e.g. inflammation, infection or  
PT cancer.  
PS Claim 2; SEQ ID NO 4; 36bp; English.  
XX  
XX The invention relates to an isolated or recombinant nucleic acid encoding  
CC interleukin-1zeta polypeptide. The invention is useful in gene therapy.  
CC The composition and methods are useful in diagnosing or treating  
CC degenerative or abnormal conditions which directly or indirectly involve  
CC development, differentiation or function, e.g. of the immune system  
CC and/or haematopoietic cells. The invention may also be used for  
CC preventing or treating other diseases or disorders associated with  
CC abnormal expression or triggering of response to the interleukin, such as  
CC inflammatory disorders, infection, allergies or cancer. The present  
CC sequence is human interleukin-1zeta variant.  
XX  
SQ Sequence 218 AA;

#### Alignment Scores:

Pred. No.:	1,34e-93	Length:	218
Score:	895.00	Matches:	169
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.92%	Indels:	0
DB:	8	Gaps:	0

US-09-869-566-4 (1-650) X ADJ88306 (1-218)

QY 112 CCAAGGTGAAGACTTAAACCGAAGAAATTGAGATTGATGACCAAGATCAAAAGTA 171  
DB 50 ProlysValIysAsnLeuAsnProIysPheSerIleHisAspGlnAspHisIysVal 69  
QY 172 CTGGTCTCTGAGCTCTGGAGATCTCATAGAGAGTTCCAGATAAACATACAGCCAGAG 231  
DB 70 LeuValIeuAspSerIleuAsnLeuIleAlaValProAspIysAsnIleAlaGProGlu 89  
QY 232 ATCTTCTTTGCAATTAGCTTCATCTTGAAGCTGAGCTGCGGAGAAAGAGTCCGATT 291  
DB 90 IlePhePheAlaIleuAlaSerSerIleuSerSerIleAlaGluIysGlySerProIle 109  
QY 292 CTCCTGGGGGTCTCTTAAAGGGAGTTTGTCTTACTGACAGCAAGATTAAGACAAGT 351  
DB 110 LeuLeuGlyValSerIysGlyIuPheCysLeuIlyrCysAspIysAspIysGlyIuSer 129  
QY 352 CATCCATCCCTTACGTGAAGAAAGAGAACTGATGAGCTGGCCCAAAAGAAATCA 411  
DB 130 HisProSerLeuIleuIlySlySlyIySleuMetIysLeuAlaIleGlnIySlyIuSer 149  
QY 412 GCACGCCGCCCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACAATGCTGAGTGC 471  
DB 150 AlaArgArgProPheIlePheIlePheIleArgAlaGlnValGlySerIlePheMetIeuGlyIuSer 169  
QY 472 GCGGCTACCCCGAGATGTTCACTGACCTCTGCAATTGATAGAGCTGTGGGGTG 531  
DB 170 AlaAlaHisProGlyIlePheIleCysIleHisSerCysAsnGlyAsnGluProValGlyVal 189  
QY 532 ACAGATAATTTGAGAACAGGAACACATTTTCATTTCAACAGATTTGCAAAAGT 591  
DB 190 ThrAspIysPheGluAsnArgIySlyHisIleGluIyPheSerPheGlnProValCysIySlyAla 209  
QY 592 GAAATGAGCCCCAGTGAAGTCAAGCGAT 618  
DB 210 GluMetSerProSerGluValSerAsp 218



Search completed: May 28, 2005, 17:35:18  
Job time : 95 secs

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QY 233 ATCTTCTTGAATTAACCTCATCTTGAAGCTCAGCCTTCGCGAGAAAGAAATCCGATT 291
|||
DB 90 IIEPHEPHEALALEUHLASERISERISERIALAGLULYSGLYSERPROILE 109
|||
QY 292 CTCCTGGGGGTCTCTAAAGGAGGTTTGTCTTACTGTGACAAAGATAAAGCAAAAT 351
|||
DB 110 LEULEUGLYVALSERISYSGLYGUPHECYSEUITYCYASPLYSAPLSYSGLYGINSER 129
|||
QY 352 CATCCATCCCTTCAGCTGAAGAAAGAAAGTGAAGCTGCTCCCAAGAAAGAAATCA 411
|||
DB 130 HISPPOSERLEUGLNULEULYSGLULYSLEUMETLYSLEUALALAGLULYSGLYSER 149
|||
QY 412 GCAGCCGCGCCCTTCATCTTTATAGAGCTCAGTGGGCTCTGGAACATGCTGAGTGC 471
|||
DB 150 ALAARGARGPROPHLEIIEPHEITYRARGLAGLNUVALGYSERTPRASMETLEUGLINSER 169
|||
QY 472 GCGGCTCACCCCGAGATGTTGATCTGACCTCTCGAATTTGATATAGAGCTGTGGGGTG 531
|||
DB 170 ALAALAHASPROGLYTRPHEILECYSTRISERCYASNCYSASNGLUPROVALGLYVAL 189
|||
QY 532 ACAGATTAATTTGAGAAACAGAAACATTTGAATTTTCATTTCAACAGTTTGCAAAAGCT 591
|||
DB 190 THIASPLYPHEGLULASNGLYSHISILEGLUPHESERPHGLINPROVALCYSLYSALA 209
|||
QY 592 GAAATGAGCCCGCAGTGAGGTCAGCGAT 618
|||
DB 210 GLUMETSERPROSERGLUVALSERASP 218
|||
RESULT 2
US-09-398-412B-4
; Sequence 4, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 218
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-398-412B-4

Alignment Scores:
Pred. No.: 5,49e-99 Length: 218
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: 4 Gaps: 0

US-09-869-566-4 (1-650) x US-09-398-412B-4 (1-218)
QY 112 CCAAGGTGAAGAACTTAAACCCGAAAGAAATTGACATTCATGACCAAGATCAAAAGTA 171
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DB 50 PROLYVALLYSASNLEULASNPROLYSLYPHESERILEHISAPGLINAPHISLVSVAL 69
|||
QY 172 CTGGTCTCTGAGCTCTGGAATCTCATAGCAGTTCCAGATTAACATCACTACCCCGAGG 231
|||
DB 70 LEUVALLEUASPSERGLYSNLEULLEAVALPROASPLYSASNLYRILEARGPROGLU 89
|||
QY 232 ATCTTCTTGAATTAACCTCATCTTGAAGCTCAGCCTTCGCGAGAAAGAAATCCGATT 291
|||
DB 90 IIEPHEPHEALALEUHLASERISERISERIALAGLULYSGLYSERPROILE 109
|||
QY 292 CTCCTGGGGGTCTCTAAAGGAGGTTTGTCTTACTGTGACAAAGATAAAGCAAAAT 351
|||
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DB 110 LEULEUGLYVALSERISYSGLYGUPHECYSEUITYCYASPLYSAPLSYSGLYGINSER 129
|||
QY 352 CATCCATCCCTTCAGCTGAAGAAAGAAAGTGAAGCTGCTCCCAAGAAAGAAATCA 411
|||
DB 130 HISPPOSERLEUGLNULEULYSGLULYSLEUMETLYSLEUALALAGLULYSGLYSER 149
|||
QY 412 GCAGCCGCGCCCTTCATCTTTATAGAGCTCAGTGGGCTCTGGAACATGCTGAGTGC 471
|||
DB 150 ALAARGARGPROPHLEIIEPHEITYRARGLAGLNUVALGYSERTPRASMETLEUGLINSER 169
|||
QY 472 GCGGCTCACCCCGAGATGTTGATCTGACCTCTCGAATTTGATATAGAGCTGTGGGGTG 531
|||
DB 170 ALAALAHASPROGLYTRPHEILECYSTRISERCYASNCYSASNGLUPROVALGLYVAL 189
|||
QY 532 ACAGATTAATTTGAGAAACAGAAACATTTGAATTTTCATTTCAACAGTTTGCAAAAGCT 591
|||
DB 190 THIASPLYPHEGLULASNGLYSHISILEGLUPHESERPHGLINPROVALCYSLYSALA 209
|||
QY 592 GAAATGAGCCCGCAGTGAGGTCAGCGAT 618
|||
DB 210 GLUMETSERPROSERGLUVALSERASP 218
|||
RESULT 3
US-09-398-412B-2
; Sequence 2, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-398-412B-2

Alignment Scores:
Pred. No.: 3,43e-95 Length: 218
Score: 863.50 Matches: 172
Percent Similarity: 87.19% Conservative: 5
Best Local Similarity: 84.73% Mismatches: 11
Query Match: 76.15% Indels: 15
DB: 4 Gaps: 2

US-09-869-566-4 (1-650) x US-09-398-412B-2 (1-218)
QY 55 GACTACAAAGAGATGACGACAAAGCTTGGC-----GCCCGCAATTCAGCTCTTGGC 105
|||
DB 16 ASPTIRPGLULYASDPLUPROGLNLCYSYSEUGLUNASPROLAGLISERTROLEUGLU 35
|||
QY 106 AGAGTGAAGAACTTA-----AAGGTGAAGAACTTA 129
|||
DB 36 PROGLYPROSERLEUPROTHRMECLAMPHEVALHISHTHSERARGLYSVALYSSERLEU 55
|||
QY 130 AACCCGAGAAATTTGACATTCATGACCAAGATCAAAAGTACTGTCTGAGCTCTGGG 189
|||
DB 56 AENPROLYLYLPHESEERILEHISAPGLINAPHISLVSVALLEUVALLEUASPSERGLY 75
|||
QY 190 AATCTCATAGCAGTTCCAGATTAACATCACTACGCCAGAAATCTTCTTGTGATTAAGCC 249
|||
DB 76 AENLEULLEAVALPROASPLYSASNLYRILEARGPROGLULIEPHEPHEALALEUALA 95
|||
QY 250 TCAATCTTGAAGCTCAGCTCTGCGAGAAAGAAAGTCCGATTCCTCGGGGGTCTTAA 309
|||
DB 96 SERISERISERIALAGLULYSGLYSERLEULEULEUGLYVALSERLYS 115
|||
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QY 310 GGGAGTTTGTCTTACTGTGACAAAGATTAAGACAAAGTCATCCCTTCAGCTG 369
DB 116 GtlyGluPheCysLeuTyrcysAspLyAspLyGtlyGlnSerHisProSerLeuGlnLeu 135
QY 370 AAGAAAGAAATATGATGAAGCTGCTGCCAAAGAAATGACAGCCGCGCTTCATC 429
DB 136 LysLysGtlyLysLeuMetLysLeuAlaGlnLysGlnSerLysArgProPheile 155
QY 430 TTTTAAAGGCTCAGGTGGGCTCTGGAATCATGTGAGTGGGCTGACCCCGGATG 489
DB 156 PheTyrcysAlaGlnAlaGtlySerArgMetLeuGlnSerLysAlaHisProGlyTyr 175
QY 490 TTTCATCTGCACCTCTCTGCAATTTGTAATGAGCCCTGTGGGCTGACAGATTAATTGAGAAC 549
DB 176 PheileCysTherSerCysAsnCyAsnGlnProValGlyValThrAspLysPheGlnLeu 195
QY 550 AAGAAACACATGTAATTTTCATTTTCAACCAAGTTTGCAAAAGCTGAAATGAGCCCGAGTGA 609
DB 196 ArgLysHisileGtlyPheSerPheGlnProValCysLysAlaGlnMetSerProSerGln 215
QY 610 GTCAGGAT 618
DB 216 ValSerAsp 218

RESULT 4
US-09-128-155-7
; Sequence 7, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-7

Alignment Scores:
Pred. No.: 8,88e-76 Length: 167
Score: 702.00 Matches: 131
Percent Similarity: 97.14% Conservative: 5
Best Local Similarity: 93.57% Mismatches: 4
Query Match: 61.90% Indels: 0
DB: 3 Gaps: 0

US-09-869-566-4 (1-650) x US-09-128-155-7 (1-167)
QY 199 GCAGTTCAGATTAATAACTACATACGCCCAAGATCTTTGCAATTAGCCTCATCTTG 258
DB 28 SerLeuProThrMetAsnPheValHisThrLysilePhePheAlaLeuAlaSerSerLeu 47
QY 259 AGCTCAGCTCTGCGGAGAAAGAAAGTCCGATTTCTCTGGGGGTCTCTAAAGGGAGTTT 318
DB 48 SerSerAlaSerAlaGlnLysGtlySerProileuLeuGlyValSerLysGtlyGlnPhe 67
QY 319 TGTCTCTACTGTGACAAAGATTAAGACAAAGTCATCCCTTCAGCTGAAAGAGAG 378
DB 68 CysLeuTyrcysAspLysAspLysGtlyGlnSerHisProSerLeuGlnLeuLysGtly 87
QY 379 AACTGATGAGCTGGCTGCCCAAAAGAAATGACAGCGCGGCTTCATCTTTTATAG 438
DB 88 LysLeuMetLysLeuAlaGlnLysGtlySerAlaArgProPheilePheTyrcys 107
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QY 439 GCTCAGTGGGCTCTGGAACATGCTGAGTGGGCTCACCCCGATGTTTCATCTGC 498
DB 108 AlaGlnValGlySerTrpAsnMetLeuGlnSerLysAlaAlaHisProGlyTrpPheileCys 127
QY 499 ACCTCTGCAATTGTATGAGCTGTGGGCTGACAGATTAATTGAGAAACAGAAAC 558
DB 128 ThrSerCysAsnCyAsnGlnProValGlyValThrAspLysPheGlnLysArgLysHis 147
QY 559 ATTGAATTTTCATTTCAACACAGTTTGCAAAAGCTGAAATGAGCCCGAGTGCAGCAT 618
DB 148 ileGlnPheSerPheGlnProValCysLysAlaGlnMetSerProSerGlnValSerAsp 167

RESULT 5
US-09-128-155-2
; Sequence 2, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-2

Alignment Scores:
Pred. No.: 9,12e-76 Length: 178
Score: 702.00 Matches: 131
Percent Similarity: 97.14% Conservative: 5
Best Local Similarity: 93.57% Mismatches: 4
Query Match: 61.90% Indels: 0
DB: 3 Gaps: 0

US-09-869-566-4 (1-650) x US-09-128-155-2 (1-178)
QY 199 GCAGTTCAGATTAATAACTACATACGCCCAAGATCTTTGCAATTAGCCTCATCTTG 258
DB 39 SerLeuProThrMetAsnPheValHisThrLysilePhePheAlaLeuAlaSerSerLeu 58
QY 259 AGCTCAGCTCTGCGGAGAAAGAAAGTCCGATTTCTCTGGGGGTCTCTAAAGGGAGTTT 318
DB 59 SerSerAlaSerAlaGlnLysGtlySerProileuLeuGlyValSerLysGtlyGlnPhe 78
QY 319 TGTCTCTACTGTGACAAAGATTAAGACAAAGTCATCCCTTCAGCTGAAAGAGAG 378
DB 79 CysLeuTyrcysAspLysAspLysGtlyGlnSerHisProSerLeuGlnLeuLysGtly 98
QY 379 AACTGATGAGCTGGCTGCCCAAAAGAAATGACAGCGCGGCTTCATCTTTTATAG 438
DB 99 LysLeuMetLysLeuAlaGlnLysGtlySerAlaArgProPheilePheTyrcys 118
QY 439 GCTCAGTGGGCTCTGGAACATGCTGAGTGGGCTCACCCCGATGTTTCATCTGC 498
DB 119 AlaGlnValGlySerTrpAsnMetLeuGlnSerLysAlaAlaHisProGlyTrpPheileCys 138
QY 499 ACCTCTGCAATTGTATGAGCTGTGGGCTGACAGATTAATTGAGAAACAGAAAC 558
DB 139 ThrSerCysAsnCyAsnGlnProValGlyValThrAspLysPheGlnLysArgLysHis 158
QY 559 ATTGAATTTTCATTTCAACACAGTTTGCAAAAGCTGAAATGAGCCCGAGTGCAGCAT 618
DB 159 ileGlnPheSerPheGlnProValCysLysAlaGlnMetSerProSerGlnValSerAsp 178
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RESULT 6
US-09-128-155-11
: Sequence 11, Application US/09128155
: Patent No. 6117654
: GENERAL INFORMATION:
: APPLICANT: Pan, Yang
: TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
: FILE REFERENCE: 09404/052001
: CURRENT APPLICATION NUMBER: US/09/128,155
: CURRENT FILING DATE: 1998-08-03
: EARLIER APPLICATION NUMBER: US 60/091,650
: EARLIER FILING DATE: 1998-07-02
: EARLIER APPLICATION NUMBER: US 60/054,646
: EARLIER FILING DATE: 1997-08-04
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 11
: LENGTH: 136
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-128-155-11

Alignment Scores:
Pred. No.: 5.69e-75 Length: 136
Score: 695.00 Matches: 130
Percent Similarity: 98.52% Conservative: 3
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 61.29% Indels: 0
DB: 3 Gaps: 0

US-09-869-566-4 (1-650) x US-09-128-155-11 (1-136)

QY 214 AACTACGATAGCCCAAGATCTTTGGATTAAGCTCATCTTGAGCTGAGCTGCG 273
Db 2 Asnpevalahisthrlysllepehealaleualaserseusersestala 21
: :::::

QY 274 GAGAAAGAGAGTCCGATTCCTCGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 333
Db 22 GlnlyselrrolleuleuenglvalserlysglgluphecylenlyrCyasp 41

QY 334 AAGATTAAGACAAAGTCATCCCTTCAGCTGAAGAGAGAACTATAGACTG 393
Db 42 LysaspysglglinsertisproserleuglnleuylsglulyleuMetylsleu 61

QY 394 GCTGCCAAAGGAATCAGACGCGCGCTTCATCTTTTAAAGGCTCAGTGGCTCC 455
Db 62 AlaladlnlsgluseralalargatgProphellepheTyTArgalaglnvalglyser 81

QY 454 TGGAAACATGCTGAGATCGGGGCTCACCCGGATGGTTCATCGACCTCCGCAATTGT 513
Db 82 TrpasmleuleulseralalahlsproglyTrrpheillecythserCyahsnCyS 100

QY 514 AATGAGCTGTGTGGGTGACAGATAATTGTGAAGACAGAAACACATGGAATTTGATT 573
Db 102 AsngluprovalgllyalThrdsrlyspRegluasArglynhlslleglupheserphe 121

QY 574 CAACCAAGTTGCAAAAGCTGAATAAGACCCCAAGTGAAGCTCAGGAT 618
Db 122 GlnprovalCyhsylasalaaglnumetserProserglulvalserasp 136

RESULT 7
US-09-128-155-5
: Sequence 5, Application US/09128155
: Patent No. 6117654
: GENERAL INFORMATION:
: APPLICANT: Pan, Yang
: TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
: FILE REFERENCE: 09404/052001
: CURRENT APPLICATION NUMBER: US/09/128,155
: CURRENT FILING DATE: 1998-08-03

```

	/ EARLIER APPLICATION NUMBER: US 60/091,650	
	/ EARLIER FILING DATE: 1998-07-02	
	/ EARLIER APPLICATION NUMBER: US 60/054,646	
	/ EARLIER FILING DATE: 1997-08-04	
	/ NUMBER OF SEQ ID NOS: 18	
	/ SOFTWARE: FastSeq for Windows Version 3.0	
	/ SEQ ID NO 5	
	/ LENGTH: 115	
	/ TYPE: PRT	
	/ ORGANISM: Homo sapiens	
	US-09-128-155-5	
 Alignment Scores:		
Pred. No.:	2,52e-66	Length: 115
Scores:	623.00	Matches: 115
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	54,94%	Indels: 0
DB:	3	Gaps: 0
 US-09-869-566-4 (1-650) x US-09-128-155-5 (1-115)		
OY	274 GAGAAAGAATGCCGATTCTCCTGGCGGTCTCTAAGGGAGTTTGTCTCTACTGTGAC	333
Db	1 GlutylgliserProleuleuengllyalserlsglyglunphcysleutyCyasp	20
OY	334 AAGATTAAGACAANAAGTATCATTCCTTGACGTGAAGAAAGAAAACGTATGAACCTG	393
Db	21 Lysasplysdlglserhsrproserleuglnleulslysglylslemetlslenu	40
OY	394 GCAGCCCAAAAGGAATCACAGCCGCGGCCTTCATCTTTTADAGAGGCTCAGGTGGCTCC	453
Db	41 Alahlaclimsgluserlalaratgrrprohellereptyrahalaglnvalglyser	60
OY	454 TGAACATGCTGGAGTCGCGCGGCTCAACC CGGATGTTTCATCTGCACCTCTCGCAATTGT	513
Db	61 TrpasmterleucluserlalalahsproglyttrphenelicystlnserCyasnCys	80
OY	514 AATGAGCCTGTTGGGGGTGACAGATAATTTGAGAACAGGAAACACATTGATTTTCAATT	573
Db	81 AsngluprovalgllyalThrapslysrPneglunamalgvlshsllegluPheserPhe	100
OY	574 CAACCAAGTTGCAAGCTGAATGAAGCCCGAGTAGTGCAGCGAT	618
Db	101 GlmprovalCyslslaslagnlmetserProserglunalserAsp	115
 RESULT 8		
US-09-128-155-9		
Sequence 9, Application US/09128155		
Patent No. 6117654		
GENERAL INFORMATION:		
APPLICANT: Pan, Yang		
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY		
TITLE OF INVENTION: AND USES THEREOF		
FILE REFERENCE: 09404/052001		
CURRENT APPLICATION NUMBER: US/09/128,155		
CURRENT FILING DATE: 1998-08-03		
EARLIER APPLICATION NUMBER: US 60/091,650		
EARLIER FILING DATE: 1998-07-02		
EARLIER APPLICATION NUMBER: US 60/054,646		
EARLIER FILING DATE: 1997-08-04		
NUMBER OF SEQ ID NOS: 18		
SOFTWARE: FastSeq for Windows Version 3.0		
SEQ ID NO 9		
LENGTH: 115		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-09-128-155-9		
 Alignment Scores:		
Pred. No.:	2,52e-66	Length: 115
Scores:	623.00	Matches: 115
Percent Similarity:	100.00%	Conservative: 0

Best Local Similarity: 100.00%  
Query Match: 54.94%  
DB: 3  
Gaps: 0  
US-09-869-566-4 (1-650) x US-09-128-155-9 (1-115)

QY 274 GAGAAAGAAAGTCCGATTCCTCGGGGCTCTAAAGGAGATTGTTCTCTACTGTGAC 333  
DB 1 GlnlyGlySerProIleuLeuGlyValSerlyGlyGluPheCysLeuTyrCysAsp 20  
QY 334 AAGGATTAAGGACAAAGTCAATCCCTTCAGCTGAAGAGAAAGAACTGATGAAGCTG 393  
DB 21 LysAspLysGlyGlnSerHisProSerLeuGlnLeuLysGlyLysLeuMetLysLeu 40  
QY 394 GCTGCCCAAGGAAATCAGACGCCGCCCTTCATCTTTATAGGCTCAGTGGGCTCC 453  
DB 41 AAlaGlnLysLeuSerAlaAlaHisProGlyTyrPheLleCysThrSerCysAsnCys 60  
QY 454 TGGAAATGCTGAGTGGGGCTCAACCCGATGGTTCACTGACCTCTGCAATTGT 513  
DB 61 TrpAsnMetLeuGlnSerAlaAlaHisProGlyTyrPheLleCysThrSerCysAsnCys 80  
QY 514 AATGACCTGTGGGTGACAGATAATTTAGAACAGAAACATTAATTTTCATT 573  
DB 81 AasnGlnProValGlyValThrAspLysPheGlnAsnArgLysHisLleGlnPheSerPhe 100  
QY 574 CAACGATTGCAAGCTGAATGAGCCCGCAGTGAAGTCCAGCAT 618  
DB 101 GlnProValCysLysAlaGlnMetSerProSerGlnValSerAsp 115

RESULT 9  
US-09-128-155-13  
Sequence 13, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-128-155-13

Alignment Scores:  
Pred. No.: 2,52e-66 Length: 115  
Score: 623.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 54.94% Indels: 0  
DB: 3 Gaps: 0

US-09-869-566-4 (1-650) x US-09-128-155-13 (1-115)  
QY 274 GAGAAAGAAAGTCCGATTCCTCGGGGCTCTAAAGGAGATTGTTCTCTACTGTGAC 333  
DB 1 GlnlyGlySerProIleuLeuGlyValSerlyGlyGluPheCysLeuTyrCysAsp 20  
QY 334 AAGGATTAAGGACAAAGTCAATCCCTTCAGCTGAAGAGAAAGAACTGATGAAGCTG 393  
DB 21 LysAspLysGlyGlnSerHisProSerLeuGlnLeuLysGlyLysLeuMetLysLeu 40  
QY 394 GCTGCCCAAGGAAATCAGACGCCGCCCTTCATCTTTATAGGCTCAGTGGGCTCC 453

DB 41 AAlaGlnLysLeuSerAlaAlaHisProPheLlePheTyrArgAlaGlnValGlySer 60  
QY 454 TGGAAATGCTGAGTGGGGCTCAACCCGATGGTTCACTGACCTCTGCAATTGT 513  
DB 61 TrpAsnMetLeuGlnSerAlaAlaHisProGlyTyrPheLleCysThrSerCysAsnCys 80  
QY 514 AATGACCTGTGGGTGACAGATAATTTAGAACAGAAACATTAATTTTCATT 573  
DB 81 AasnGlnProValGlyValThrAspLysPheGlnAsnArgLysHisLleGlnPheSerPhe 100  
QY 574 CAACGATTGCAAGCTGAATGAGCCCGCAGTGAAGTCCAGCAT 618  
DB 101 GlnProValCysLysAlaGlnMetSerProSerGlnValSerAsp 115

RESULT 10  
US-09-128-155-18  
Sequence 18, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 18  
LENGTH: 185  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: synthetically generated  
LOCATION: (1)...(185)  
OTHER INFORMATION: human sequence predicted using an alignment algorithm which  
OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(185)  
OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-128-155-18

Alignment Scores:  
Pred. No.: 3,18e-48 Length: 185  
Score: 473.50 Matches: 90  
Percent Similarity: 94.90% Conservative: 3  
Best Local Similarity: 91.84% Mismatches: 4  
Query Match: 41.75% Indels: 1  
DB: 3 Gaps: 1

US-09-869-566-4 (1-650) x US-09-128-155-18 (1-185)  
QY 244 TTAGCCTCATCTTGAAGTCACTCTGCGAGAAAGAAAGTCCGATTCCTCGGGGCTC 303  
DB 71 LeuSerSerLeuGlnArgSerAlaSerAlaGlnLysGlySerProIleuLeuGlyVal 90  
QY 304 TCTAAAGGAGGAGTTTGTCTTACTGTGACAGATAAGAAAGAAAGTCAATCCCTT 363  
DB 91 SerLysGlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSerHisProSerLeu 110  
QY 364 CAGCTGAAGAGAGAAAGTGAAGCTGGTCCCAAGAGATTCAGACGGCGCC 423  
DB 111 GlnLeu---LysGlnLysLeuMetLysLeuAlaAlaGlnLysGlnSerAlaArgAspPro 129  
QY 424 TTCACTTTTATAGGCTCAGTGGGCTCTGGAACATGCTGAGTGGCGGCTCAACCC 483  
DB 130 PheLlePheTyrArgAlaGlnValGlySerTrpAsnMetLeuGlnSerAlaAlaHisPro 149

QY 484 GGATGATTCATCTGCACCTCTGCAATTGTAATGAGCCTGTGGGTGACAGAT 537  
 |||||  
 Db 150 GYTPPhelleCysHserCysaencySaenglProvalGlyle\*\*asn 167

## RESULT 11

US-08-790-032-2  
 ; Sequence 2, Application US/08790032  
 ; Patent No. 5863769  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Peter  
 ; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist  
 ; TITLE OF INVENTION: Beta (IL-1RA\_)  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406-0939  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/790,032  
 ; FILING DATE: 28-JAN-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Schreck, Patricia A  
 ; REGISTRATION NUMBER: 33,777  
 ; REFERENCE/DOCKET NUMBER: ATG50051  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-270-5031  
 ; TELEFAX: 610-270-5090  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 169 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-790-032-2

## Alignment Scores:

Pred. No.: 7,73e-19 Length: 169  
 Score: 229.50 Matches: 56  
 Percent Similarity: 53.12% Conservative: 29  
 Best Local Similarity: 35.00% Mismatches: 62  
 Query Match: 20.24% Indels: 13  
 DB: 2 Gaps: 5

US-09-869-566-4 (1-650) x US-08-790-032-2 (1-169)

QY 64 GACGATGACGACAAGCTTGGCGCGCGAATTGCTTTGAGAGGTCCAAAGTGAAG 123  
 |||||  
 Db 7 AsplaAlaSpolYglYglYhAlaValTYRGlInSerMetCysLys----- 21  
 QY 124 AACTTAACCCGAGAAATTACGATTCATGACGAGATGACAAAGTACTGGTCTGGAC 183  
 |||||  
 Db 22 -----ProleThrglYthrIleAsnAspLeuAsnInglInValItrPrhLeuGln 38  
 QY 184 TCTGGAATCTCATGAGCTTCCAGATTAATAAACTACATACCCGAGAGATCTTTGCA 243  
 |||||  
 Db 39 GlyGlnAsnLeuValAlaValProArGserAspSerValThrProValItrValAlaVal 58  
 QY 244 TTAGCTCATCTTGGAGCTGAGCTCTGCGAG--AAAGAAATCGGATTTCTCGGGG 300  
 |||||

Db 59 IlleThrCysLysTYrProGlnAlaLeuGlnGlnYlArGlyAspProIleTYrLeuGly 78  
 QY 301 GTCCTAAAGGGAGATTGTGTCTACTGTGACAAGATTAAGCAAAAGTCATCATCC 360  
 |||||  
 Db 79 IlleGlnAsnProGlnMetCysLeuTYrCysGlnYlValGlyGln-----Prothr 96  
 QY 361 CTTGAGCTGAGAGAGAGAACTGATGAAGCTGCTGCCAAAGAAAGAACTACAGCCGCG 420  
 |||||  
 Db 97 LeuGlnLeuYlGlnGlnYlMetAspLeuTYrGlyGlnProGlnProVal---Lys 115  
 QY 421 CCCTTCATCTTTAAGGCTGAGGTGGCTCTCGGAACATGCTGAGTGGCGGCTGAC 480  
 |||||  
 Db 116 ProPheLeuPheTYrAlaYlArGlyThrGlyArGThrSerThrLeuGlnSerValAlaPhe 135  
 QY 481 CCCGATGATTCATCTGCACCTCTGCAATTGTAATGAGCCTGTGGGTGACAGATTA 540  
 |||||  
 Db 136 ProAspTPPhelleAlaLaser--LysArGAspGlnProIleIleuThrSerGlu 154

## RESULT 12

US-09-069-619-2  
 ; Sequence 2, Application US/09069619  
 ; Patent No. 6054559  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Peter and Lisa Marshall  
 ; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist  
 ; TITLE OF INVENTION: Beta (IL-1RA\_)  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406-0939  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/069,619  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/007,464; and 08/790,032  
 ; FILING DATE: filed 14-JAN-1998; and 28-JAN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Han, William, T.  
 ; REGISTRATION NUMBER: 34,344  
 ; REFERENCE/DOCKET NUMBER: ATG50051-2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-270-5219  
 ; TELEFAX: 610-270-5090  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 169 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-069-619-2

## Alignment Scores:

Pred. No.: 7,73e-19 Length: 169  
 Score: 229.50 Matches: 56  
 Percent Similarity: 53.12% Conservative: 29  
 Best Local Similarity: 35.00% Mismatches: 62  
 Query Match: 20.24% Indels: 13  
 DB: 3 Gaps: 5

US-09-869-566-4 (1-650) x US-09-069-619-2 (1-169)



QY 64 GACGATGACGACAGCTGGCGCGCGGAATTAGCTCTTTGACAGAGTCCAAAGTGAAG 123  
|||  
|||  
7 AapAlaaspGlyGlyYrGlnValYrGlnSerMetCysLys----- 21  
QY 124 AACTTAACCCGAGAAATTGACATTCATGACACGAGATCAAAAGTACTGCTCTGAC 183  
|||  
|||  
22 -----ProIleThrGlyThrIleAsnAspLeuAsnGlnValIleThrLeuGln 38  
QY 184 TCTGGGAATCTCATAGCTGCTCCAGATTAATACTACATAGCCGACAGATCTTTTGA 243  
|||  
|||  
39 GlyIleAsnLeuValAlaValProArgSerAspSerValThrProValThrValAlaVal 58  
QY 244 TTAGCCTCATCTTGAAGCTCAAGCTCTGCGAG--AAAGAAAGTCCGATTCTCTGCGG 300  
|||  
|||  
59 IleThrCysLeuTyrrProGlnIleAsnGlnGlnGlnIleArgGlyAspProIleTyrrLeuGly 78  
QY 301 GCTCTTAAGGAGAGTTTGTCTCTACTGTGACAAAGATTAAGAGCAAAATCATCTCC 360  
|||  
|||  
79 IleGlnAsnProGlnMetCysLeuTyrrCysGlnValGlyGln-----ProThr 96  
QY 361 CTTGAGCTGAAGAGAGAACTGATGAAGCTGCTGCCCAAAAGAGATCAGACGCCG 420  
|||  
|||  
97 LeuGlnMetLeuGlnGlnIleMetAspLeuTyrrGlyGlnProGlnProVal---Lys 115  
QY 421 CCCTTCATCTTTATAGGCTCAGTGGCTCTCGAACAATGCTGAGTGGCGGCTCAC 480  
|||  
|||  
116 ProPheLeuPheTyrrArgAlaLysThrGlyArgThrSerThrLeuGlnSerValAlaPhe 135  
QY 481 CCGGATGTTTATCTGCACTCTCGCAATTGATGAGCTGTTGGGGTGACAGATAA 540  
|||  
|||  
136 ProAspTrpPheIleAlaSerSer---LysArgAspGlnProIleIleLeuThrSerGln 154

RESULT 13  
US-09-494-018-2  
Sequence 2, Application US/09494018  
Patent No. 639573  
GENERAL INFORMATION:  
APPLICANT: Peter R. Young  
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST BETA  
FILE REFERENCE: ATG-50051-D1  
CURRENT APPLICATION NUMBER: US/09/494, 018  
CURRENT FILING DATE: 2000-01-28  
EARLIER APPLICATION NUMBER: 09/069, 619  
EARLIER FILING DATE: 1998-04-29  
EARLIER APPLICATION NUMBER: 09/007, 464  
EARLIER FILING DATE: 1998-01-14  
EARLIER APPLICATION NUMBER: 08/790, 032  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 169  
TYPE: PR  
ORGANISM: HOMO SAPIENS  
US-09-494-018-2

Alignment Scores:  
Pred. No.: 7,73e-19 Length: 169  
Score: 229.50 Matches: 56  
Percent Similarity: 53.12% Conservative: 29  
Best Local Similarity: 35.00% Mismatches: 62  
Query Match: 20.24% Indels: 13  
Gaps: 5  
US-09-869-566-4 (1-650) x US-09-494-018-2 (1-169)

QY 64 GACGATGACGACAGCTGGCGCGCGGAATTAGCTCTTTGACAGAGTCCAAAGTGAAG 123  
|||  
|||  
7 AapAlaaspGlyGlyYrGlnValYrGlnSerMetCysLys----- 21  
QY 124 AACTTAACCCGAGAAATTGACATTCATGACACGAGATCAAAAGTACTGCTCTGAC 183  
|||  
|||  
22 -----ProIleThrGlyThrIleAsnAspLeuAsnGlnValIleThrLeuGln 38  
QY 184 TCTGGGAATCTCATAGCTGCTCCAGATTAATACTACATAGCCGACAGATCTTTTGA 243  
|||  
|||  
39 GlyIleAsnLeuValAlaValProArgSerAspSerValThrProValThrValAlaVal 58  
QY 244 TTAGCCTCATCTTGAAGCTCAAGCTCTGCGAG--AAAGAAAGTCCGATTCTCTGCGG 300  
|||  
|||  
59 IleThrCysLeuTyrrProGlnIleAsnGlnGlnGlnIleArgGlyAspProIleTyrrLeuGly 78

DB 22 -----ProIleThrGlyThrIleAsnAspLeuAsnGlnValIleThrLeuGln 38  
QY 184 TCTGGGAATCTCATAGCTGCTCCAGATTAATACTACATAGCCGACAGATCTTTTGA 243  
|||  
|||  
39 GlyIleAsnLeuValAlaValProArgSerAspSerValThrProValThrValAlaVal 58  
QY 244 TTAGCCTCATCTTGAAGCTCAAGCTCTGCGAG--AAAGAAAGTCCGATTCTCTGCGG 300  
|||  
|||  
59 IleThrCysLeuTyrrProGlnIleAsnGlnGlnGlnIleArgGlyAspProIleTyrrLeuGly 78  
QY 301 GCTCTTAAGGAGAGTTTGTCTCTACTGTGACAAAGATTAAGAGCAAAATCATCTCC 360  
|||  
|||  
79 IleGlnAsnProGlnMetCysLeuTyrrCysGlnValGlyGln-----ProThr 96  
QY 361 CTTGAGCTGAAGAGAGAACTGATGAAGCTGCTGCCCAAAAGAGATCAGACGCCG 420  
|||  
|||  
97 LeuGlnMetLeuGlnGlnIleMetAspLeuTyrrGlyGlnProGlnProVal---Lys 115  
QY 421 CCCTTCATCTTTATAGGCTCAGTGGCTCTCGAACAATGCTGAGTGGCGGCTCAC 480  
|||  
|||  
116 ProPheLeuPheTyrrArgAlaLysThrGlyArgThrSerThrLeuGlnSerValAlaPhe 135  
QY 481 CCGGATGTTTATCTGCACTCTCGCAATTGATGAGCTGTTGGGGTGACAGATAA 540  
|||  
|||  
136 ProAspTrpPheIleAlaSerSer---LysArgAspGlnProIleIleLeuThrSerGln 154

RESULT 14  
US-09-398-412B-15  
Sequence 15, Application US/09398412B  
Patent No. 6680380  
GENERAL INFORMATION:  
APPLICANT: Timans, Jacqueline C.  
TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager  
FILE REFERENCE: DX0904K  
CURRENT APPLICATION NUMBER: US/09/398, 412B  
CURRENT FILING DATE: 1999-09-17  
PRIOR APPLICATION NUMBER: US 60/100948  
PRIOR FILING DATE: 1998-09-18  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 169  
TYPE: PR  
ORGANISM: Homo sapiens  
US-09-398-412B-15

Alignment Scores:  
Pred. No.: 7,73e-19 Length: 169  
Score: 229.50 Matches: 56  
Percent Similarity: 53.12% Conservative: 29  
Best Local Similarity: 35.00% Mismatches: 62  
Query Match: 20.24% Indels: 13  
Gaps: 5  
US-09-869-566-4 (1-650) x US-09-398-412B-15 (1-169)

QY 64 GACGATGACGACAGCTGGCGCGCGGAATTAGCTCTTTGACAGAGTCCAAAGTGAAG 123  
|||  
|||  
7 AapAlaaspGlyGlyYrGlnValYrGlnSerMetCysLys----- 21  
QY 124 AACTTAACCCGAGAAATTGACATTCATGACACGAGATCAAAAGTACTGCTCTGAC 183  
|||  
|||  
22 -----ProIleThrGlyThrIleAsnAspLeuAsnGlnValIleThrLeuGln 38  
QY 184 TCTGGGAATCTCATAGCTGCTCCAGATTAATACTACATAGCCGACAGATCTTTTGA 243  
|||  
|||  
39 GlyIleAsnLeuValAlaValProArgSerAspSerValThrProValThrValAlaVal 58  
QY 244 TTAGCCTCATCTTGAAGCTCAAGCTCTGCGAG--AAAGAAAGTCCGATTCTCTGCGG 300  
|||  
|||  
59 IleThrCysLeuTyrrProGlnIleAsnGlnGlnGlnIleArgGlyAspProIleTyrrLeuGly 78

```

QY 301 GTCTCTAAGGGAGTTTGTCTACTGTGACAAAGATTAAGCAAAATCATTCATCC 360
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 79 IEGlnAsnProGlnuMetCysLeuTYrCysGluValGlyGluIn-----ProThr 96
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 CTTTCAGCTAAGAGAGAAAGAACTGATGAAGCTGGCTGCCCAAAAGAAATCAGACGCCCG 420
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 97 LeuGlnLeuLysGluInLysIleMetAspLeuTYrGlyGlnProGlnProVal--Lys 115
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 CCGTCATCTTTTATATAGGCTCAGTGGGCTCCTCGAACAATGCTGGAGTCGGCGGCTCAC 480
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 ProPheLeuPheTYrThrGlnAlaLysThrGlyArgThrSerThrLeuGlnSerValAlaPhe 135
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 CCGGATGCTTCATCTGCACCTCTGCAATTGTAATGACCTGTGGGGTGCACAGATAAA 540
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 136 ProAspTYrPheIleAlaSerSer--LysArgAspGlnProIleIleLeuThrSerGlu 154
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 15

```

US-09-976-472A-2
; Sequence 2, Application US/09976472A
; Patent No. 6753166
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: RENSHAM, Blair R.
; TITLE OF INVENTION: IL-1 ETA DNA AND POLYPEPTIDES
; FILE REFERENCE: 2932-B
; CURRENT APPLICATION NUMBER: US/09/976,472A
; PRIOR APPLICATION NUMBER: PCT/US00/14435
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/162,331
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/135,758
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-976-472A-2

```

```

Alignment Scores:
Pred. No.: 8.61e-19 Length: 157
Score: 229.00 Matches: 47
Percent Similarity: 59.26% Conservative: 33
Best Local Similarity: 34.81% Mismatches: 51
Query Match: 20.19% Indels: 4
DB: 4 Gaps: 3

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US-09-869-566-4 (1-650) x US-09-976-472A-2 (1-157)

```

QY 133 CCGAAGAATTTCAGATTCATGACGAGATCACAAAATGATCTGGTCTGGACTTGGGAAT 192
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 9 ProLysSerTYrAlaIleArgAspSerArgGlnMetValTYrValLeuSerGlyAsnSer 28
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 193 CTCATAGCAGTTCCAGATAAACTACATACGCCCAAGATCTTCTTGCATTAGCC-- 249
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 29 LeuIleAlaIleProLeuSerArgSerIleLysProValThrLeuHisLeuIleAlaCys 48
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 250 TCATCTTGAAGCTCAGCCTCTGCGAAGAAAGAAATGCCATTCTCTGGGGGTCTCTAAA 309
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 49 ArgAspThrGlnPheSerAspLysGlnLysGlyAsnMetValTYrLeuGlyIleLysGly 68
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 310 GGGGATTTTGTCTCTACTGTGACAAAGATTAAGCAAAAGTCAATCCCTTCAGCTG 369
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 69 LysAspLeuCysLeuPheCysAlaGluIleGlnGlyLys-----ProThrLeuGlnLeu 86
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 370 AAGAAGAGAAAGAACTGATGAAGCTGCTGCCAAAGAAATCAGACGCCGCCCTTCATC 429
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 87 LysGlnLysAsnIleMetAspLeuTYrValGlnLysLys---AlaGlnLysProPheLeu 105
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 430 TTTTATAGGCTCAGGTGGCTCTCTGAAACATGCTGGAGTCGGCGGCTCACCCCGATGG 489
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 106 PhePheHisAsnLysGluGlySerThrSerValPheGlnSerValSerTYrProGlyTYr 125
QY 490 TTCATCTGCACCTCCTCGCAATTGTAATGAGCCTGTTGGGGTGACA 534
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 126 PheIleAlaThrSerThrThrSerGlyGlnProIlePheLeuThr 140
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: May 28, 2005, 17:41:22  
Job time : 42.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Comphen Ltd.

OM nucleic - protein search, using frame\_plus\_r2p model

Run on: May 28, 2005, 17:20:26 ; Search time 30 Seconds  
(without alignments)  
4169.393 Million cell updates/sec

Title: US-09-869-566-4  
Perfect score: 1134  
Sequence: 1 taattcacatgctcgcact.....cgactctagagatcccg99 650

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame\_r2p.model -DEV=xlp  
-O=/cgn2\_1/USPTO\_SPOOL\_P/US09869566/runat\_27052005\_163131\_19922/app\_query.fasta\_1.839  
-DB=PIR\_79 -OPMT=fastan -SUFFIX=rpr -MIMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bites -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09869566@CN\_1\_1\_38@runat\_27052005\_163131\_19922 -NCPU=6 -ICPU=3  
-NO\_WMAP -LANG=ENGLISH -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WAPR TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	174.5	15.4	155	2	JC7104	interleukin-1 rece
2	167	14.7	178	2	A44610	interleukin-1 rece
3	161	14.2	180	2	A39386	interleukin-1 rece
4	158.5	14.0	177	2	A30368	interleukin-1 rece
5	154.5	13.6	177	2	A54377	interleukin-1 rece
6	146.5	12.9	178	2	C40956	interleukin-1 rece
7	135.5	11.9	267	2	S38373	interleukin-1 beta
8	131.5	11.6	266	1	S23010	interleukin-1 beta
9	121.5	10.7	267	1	JN0724	interleukin-1 beta
10	120.5	10.6	269	1	IS5969	interleukin-1 beta
11	118	10.4	266	1	IC8018	interleukin-1 beta
12	98	8.6	269	1	IC801B	interleukin-1 beta
13	95.5	8.4	246	2	B25528	trypsin (EC 3.4.21
14	92.5	8.2	268	1	A30584	interleukin-1 beta

15	91	8.0	404	2	S34031	IKT3 protein - yea
16	89.5	7.9	214	2	JC5646	interleukin-1 beta
17	89.5	7.8	1250	1	B45219	N-methyl-D-asparta
18	88	7.7	466	2	T33574	hypothetical prote
19	84	7.4	270	1	ICMS1	interleukin-1 alpha
20	84	7.4	432	2	S41956	rad3 protein - Sch
21	83.5	7.4	776	2	S67053	probable membrane
22	83	7.3	845	2	T17291	hypothetical prote
23	82.5	7.3	246	1	TRRT1	trypsin (EC 3.4.21
24	82.5	7.2	393	2	E70767	hypothetical prote
25	82.5	7.3	513	2	T37806	probable flavoproc
26	81	7.1	320	2	A81434	molybdenum cofacto
27	81	7.0	686	2	E87490	NADH dehydrogenase
28	81	7.1	245	1	B96592	hypothetical prote
29	80.5	7.1	246	1	TRRT2	trypsin (EC 3.4.21
30	80.5	7.0	1142	2	T00022	B120 protein - hum
31	79.5	6.9	510	2	A42750	insulinoma-associat
32	79.5	7.0	740	2	F71369	conserved hypothet
33	79.5	6.9	1357	2	T29265	hypothetical prote
34	79	6.9	682	2	F83228	hypothetical prote
35	78.5	6.9	244	2	F90419	hypothetical prote
36	78	6.9	493	2	A87459	cytosol aminopepti
37	78	6.9	1277	2	E70224	hypothetical prote
38	78	6.8	2910	2	T42214	otogelin - mouse
39	77.5	6.8	426	2	C75297	probable protein s
40	77.5	6.7	490	2	E71486	probable s/t prote
41	77.5	6.7	757	2	T15149	hypothetical prote
42	77.5	6.8	1116	2	T31432	K-CI cotransport p
43	77	6.7	427	2	A53798	58K membrane-assoc
44	77	6.7	507	2	S25831	myocyte-specific e
45	77	6.8	859	2	C87358	hypothetical prote

ALIGNMENTS

RESULT 1  
JC7104  
interleukin-1 receptor antagonist - human  
C/S:Species: Homo sapiens (man)  
C/Date: 03-Dec-1999 #seqname\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
R/Mullero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, J.  
Biochem. Biophys. Res. Commun. 263, 702-706, 1999  
A>Title: IL1H1: A novel interleukin-1 receptor antagonist gene.  
A/Reference number: JC7104; M01D:99443727; PMID:10512743  
A/Accession: JC7104  
A/Molecule type: mRNA  
A/Residues: 1-155 <MULT>  
A/Cross-references: UNIPROT:Q9UBH0; GB:AF186094; NID:ig6049804; PIDN:AAF02757.1; PID:ig6045  
C/Genetics:  
A/Name: IL1H1  
A/Map position: 2q14  
C/Keywords: macrophage

Alignment Scores:

Pred. No.: 145e-09 Length: 155  
Score: 174.50 Matches: 54  
Percent Similarity: 42.60% Conservative: 18  
Best Local Similarity: 31.95% Mismatches: 48  
Query Match: 15.39% Indels: 49  
DB: 2 Gaps: 7

US-09-869-566-4 (1-650) x JC7104 (1-155)  
QY 91 AATTGAGCTCTTTCGAGAGTCCAAAGGTGAAGACTTAACCCGAGAAATTCAGACTT 150  
DB 4 SerGylAlaLeuCys-----PheArgMet 11  
QY 151 CATGACCAAGATCAACAAGTACTGCTCTGCACTCTGGGAATTCATAGCACTTCAGAT 210  
DB 12 LysAAspSerAlaLeuValLeuTyrlleuHisAenAnglnLeu----- 26  
QY 211 AAAAATCATATGAGCCGACAGATATCTTTCGATTAGCTCATCTTAGCTCAGCTCT 270

```

Db 27 -----LeuAlaGlyLeuHisAlaGlyLys 35
QY 271 GCGGAAAGGA-----AGT 285
Db 36 ValIleIleGlyGluGluIleSerValValProSerArgTrpLeuAspAlaSerLeuSer 55
QY 286 CCGATTCTCTGGGGGCTCTTAAAGGGAGATTGTTCTCTACTGTGACAAAGATAAGGA 345
Db 56 ProValIleLeuGlyValGlnGlySerGlnCysLeuSerCys-----GlyValGly 73
QY 346 CAAAGCATCCATCCCTTCACTGAGTGAAGAGAAACTATGAGT---GCTGCCAA 402
Db 74 Gln---GluProThrLeuThrLeuGluProValAsnIleMetGluLeuThrLeuGlyAla 92
QY 403 AAGGAATGACAGACGCGCCCTCATCTTTATAGAGGCTCAGGTGGGCTCTGGAACATG 462
Db 93 LysGluSer-----LysSerPheThrPheTyrArgArgAspMetCylLeuThrSerSer 110
QY 463 CTGAGTCTGGCGGCTCACCCCGAGTTCATCTGACCTCTGCAATTGTATGAGCCT 522
Db 111 PheGluSerAlaAlaTyrTrpGlyTrpPheLeuCysThrValProGluAlaAspGlnPro 130
QY 523 GTTGGGTACACAGATTAATTGAGAAC 549
Db 131 ValArgLeuThrGlnLeuProGluAsn 139

RESULT 2
A44610
Interleukin-1 receptor antagonist precursor - mouse
N:Alternate names: IL-1Ra
C:Species: Mus musculus (house mouse)
C:Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A44610; BA0956; A49031; I56106; I52970
R:Matsumura, H.; Rousset, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A:Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophag
A:Reference number: A44610; MUID:91316273; PMID:1830498
A:Accession: A44610
A:Molecule type: mRNA
A:Residues: 1-178 <MAT>
A:Cross-references: UNIPROT:P25085; GB:M64404; NID:9198236; PIDN:AAA3277.1; PID:9198297
R:Reisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.U.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A:Reference number: A40956; MUID:91271363; PMID:1828896
A:Accession: BA0956
A:Molecule type: DNA
A:Residues: 7-178 <BIS>
A:Cross-references: GB:M63100; NID:9198389; PIDN:AAA39310.1; PID:9198390
R:Shuck, M.E.; Bessaly, T.E.; Tracey, D.E.; Blenkowski, M.U.
Eur. J. Immunol. 21, 2775-2780, 1991
A:Title: Cloning, heterologous expression and characterization of murine interleukin 1
A:Reference number: A49031; MUID:92037824; PMID:1834470
A:Accession: A49031
A:Molecule type: mRNA
A:Residues: 23-178 <SHU>
A:Cross-references: GB:S64082; NID:9238584; PIDN:AA20265.1; PID:9238585
A:Experimental source: peritoneal macrophages, ICR strain
A:Note: sequence extracted from NCBI backbone (NCIN:64082, NCBI:P:64085)
R:Zahedi, K.; Seidlin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A:Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mapping
A:Reference number: I56106; MUID:91250712; PMID:1828262
A:Accession: I56106
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-178 <RES>
A:Cross-references: GB:M74294; NID:9198387; PIDN:AAA39309.1; PID:9198388
R:Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A:Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
A:Reference number: I52970; MUID:94271931; PMID:8003626

```

```

A:Accession: I52970
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-178 <RE2>
A:Cross-references: GB:I32838; NID:9487864; PIDN:AAA20576.1; PID:9528978
C:Genetics:
A:Gene: IL-1rn
A:Introns: 40/2; 70/1; 107/3
C:Superfamily: interleukin-1
C:Keywords: cytokine receptor
F:1-26/Domain: signal sequence #status predicted <SIG>
F:127-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>

Alignment Scores:
Pred. No.: 8.72e-09 Length: 178
Score: 167.00 Matches: 51
Percent Similarity: 46.95% Conservative: 26
Best Local Similarity: 31.10% Mismatches: 75
Query Match: 14.73% Indels: 12
DB: 2 Gaps: 7

US-09-869-566-4 (1-650) x A44610 (1-178)
QY 91 AATTGAGCTCTTGGAGAGTCCCAAGTGAAGAACTTAAACCGAAGAAATTCAGACT 150
Db 22 SerGluAlaAlaCysArgProSerGlyLysArgProCysLysMetGlnAlaPheArgIle 41
QY 151 CATGACACAGATCAACAAAGTACTGCTGCTGAGCTGGGAATCTCATAGCAGTCCAGAT 210
Db 42 TrpAspTrpArgGlnGlyThrPheTyrLeuAlaGlnAsnGlnIleAla----- 58
QY 211 AAAAATCAATACGC---CCAGAGATCTTCTTGATTAAGCTCATCTTGAAGTCAAGC 267
Db 59 ---GlyTyrLeuGlnGlyProAsnIle-----LysLeuGluGluLysIleAspMetVal 75
QY 268 TCTGGGAGAAAGAAAGTCCGATTCCTCGGGGGGCTCTAAAGGGAGCTTTGTCTTAC 327
Db 76 ProIleAspLeuHisSer---ValPheLeuGlyIleHisGlyGlyLeuGluCysLeuSer 94
QY 328 TGTGACAAAGATTAAGACAAAGTATCATCCATCCCTGAGCTGAGAGAGAAAGTATG 387
Db 95 CysAlaIleLysSerGlyAspAspIle-----LysLeuGlnLeuGluValAsnIleThr 112
QY 388 AAGCTGCTGCCCAAAAGAAATACAGACGCGCCCTTCATCTTTATAGGCTCAAGTG 447
Db 113 AspLeuSerLysAsnLysGluGluLysArg---PheThrPheIleArgSerGluLys 131
QY 448 GGCCTCTGGAACATGCTGAGTCGGCGCTCACCCCGAGTGTGATCTGACACCTCGC 507
Db 132 GlyProThrThrSerPheGluSerAlaIaCysProGlyTrpPheLeuCysThrThrLeu 151
QY 508 AATTGTAATGAGCTGTGGGTGACAGATAAATTGAGAACAGAAACACACTT---GAA 564
Db 152 GluAlaAspArgProValSerLeuThrAsnThrProGluGluProLeuIleValThrLys 171
QY 565 TTTTCATTTCAA 576
Db 172 PheTyrPheGln 175

RESULT 3
A33386
Interleukin-1 receptor antagonist, long intracellular splice form - human
N:Contains: interleukin-1 receptor antagonist, short intracellular splice form
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: I37893; A33386
R:Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Mantovani
J. Exp. Med. 182, 623-628, 1995
A:Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
A:Reference number: I37893; MUID:9555865; PMID:7629520
A:Accession: I37893
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA

```

[illegible]

Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991

A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:

A:Reference number: A40956; MUID:91271363; PMID:1828896

A:Accession: A40956

A:Molecule type: DNA

A:Residues: 1-177 <EIS>

A:Cross-references: UNIPROT:PI8510; GB:M63099; NID:g186385; PIND:AA641943.1; PID:g186386

R:Leimard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, R.

Cytokine 4, 83-89, 1992

A:Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist gene

A:Reference number: 137894; MUID:92338323; PMID:1385987

A:Accession: 137894

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-177 <LEN>

A:Cross-references: EMBL:X64532; NID:g33798; PIND:CAA45832.1; PID:g33799

R:Cartier, D.B.; Delbel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J.

J.G.; Siu, L.C.; Hardie, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrichson, R.L.; Tr

Nature 344, 633-638, 1990

A:Title: Purification, cloning, expression and biological characterization of an interle

A:Reference number: A50368; MUID:90220867; PMID:2139180

A:Accession: A50368

A:Molecule type: mRNA

A:Residues: 1-177 <CAR>

A:Note: parts of this sequence, including the amino end of the mature protein, were confi

R:Leimberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.; T

Nature 343, 341-346, 1990

A:Title: Primary structure and functional expression from complementary DNA of a human in

A:Reference number: S08160; MUID:90136921; PMID:2137201

A:Accession: S08160

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-177 <E12>

A:Cross-references: GB:X52015; NID:g32576; PIND:CAA34262.1; PID:g32577

R:Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joellin, F.G.; Dripps, D.J.; Helmdal, P.L.; Arn

Nature 343, 336-340, 1990

A:Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.

A:Reference number: S08159; MUID:90136920; PMID:2137200

A:Accession: S08159

A:Molecule type: protein

A:Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>

R:Rienkowski, M.J.; Bessalu, T.E.; Berger, A.E.; Truedell, S.E.; Shelly, J.A.; Laborde,

J. Biol. Chem. 265, 14505-14511, 1990

A:Title: Purification and characterization of interleukin 1 receptor level antagonist pri

A:Reference number: A37822; MUID:90354444; PMID:2143761

A:Accession: A37822

A:Molecule type: protein

A:Residues: 26-52;70-77;122-127;170-175 <BIE>

A:Experimental source: culture medium, PMA-stimulated THP-1 cells

C:Comment: For an alternative splice form, see PIR:A59386

C:Genetic: S

A:Gene: GDB:IL1RN

A:Cross-references: GDB:125897; OMIM:147679

A:Map position: 2q14.2-2q14.2

A:Introns: 39/2; 69/1; 106/3

C:Superfamily: interleukin-1

C:Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein

F:1-35/Domains: signal sequence #status predicted <Sig>

F:126-177/Product: interleukin-1 receptor antagonist #status experimental <Mat>

F:109/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:

Pred. No.:	6,53e-08	Length:	177
Score:	158.50	Matches:	43
Percent Similarity:	48.67%	Conservative:	30
Best Local Similarity:	28.67%	Mismatches:	66
Query Match:	13.98%	Indels:	11
DB:	2	Gaps:	6

US-09-869-566-4 (1-650) x A30368 (1-177)

91 AATTCAGCTCTTGGACGAGGTCAAAAGTGACGAAGACTTAAACCCGAAGAAATTCAGCATTT 150



QY 202 ----- GTTCCAGATAAAATCATACACGCCAGAGATCTTTGGCATTA 246  
 63 GlyProanthrinylsLeuGlululysIleAspMetValProIleAspHe----- 79  
 QY 247 GCTTCATCTTGAGCTCAGCCTCTGCGGAGAAGAGACTCGAATCTTCCTGSGGCTCT 306  
 Db 80 ----- ArgenValPheLeuGlyIleHis 87  
 QY 307 AAAGGAGATTTGCTCTACTGTGACAGAGATAAGACAAATCATCCATCCCTTCAG 366  
 Db 88 GlyGlyIysLeuCySLeuSerCysValIysSerGlyAspAspThr-----LysLeuGln 105  
 QY 367 CTGAAGAAGAGAAACTGTAGAGCTGGCTCCCAAAAGAAATAGACAGCGCGGCTTC 426  
 Db 106 LeuGlululValaenIleThrAspLeuasnIysasnIysGluIAspIlyAsArg--Phe 124  
 QY 427 ATCTTTATAGGGCTCAGGTGGGCTCTGTGAACATGCTGAGTGGCGGCTCACCCGGA 486  
 Db 125 ThrPheIleArgSerGluThrGlyProThrThrSerPheGlnSerLeuValIAspProGly 144  
 QY 487 TGGTTCAATCTGCACCTCTCGAATTTGTAATGACCTGTGTGGGGTGACAGAT 537  
 Db 145 TrpPheLeuCystrThrLeuGluIAlaAspHisProValSerLeuThrAsn 161

RESULT 7  
 S38373  
 Interleukin-1 beta precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 20-May-1994 #sequence\_rev1sion 01-Dec-1995 #text\_change 09-Jul-2004  
 C:Accession: S38373  
 R:Vanderbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde  
 Bur, J. Biochem. 217, 45-52, 1993  
 A:Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetically  
 A:Reference number: S38373; MUID:94039070; PMID:8223584  
 A:Accession: S38373  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-267 <VNA>  
 A:Cross-references: UNIPROT:Q29082; EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407975  
 C:Genetics: 16/2; 33/3; 99/1; 154/1; 197/3  
 A:Intons: Interleukin-1  
 C:Superfamily: Interleukin-1

Alignment Scores:  
 Pred. No.: 1,6e-05 Length: 267  
 Score: 135.50 Matches: 51  
 Percent Similarity: 48.30% Conservative: 34  
 Best Local Similarity: 28.98% Mismatches: 75  
 Query Match: 11.95% Indels: 16  
 Gaps: 8

US-09-869-566-4 (1-650) x S38373 (1-267)

QY 12 GTCTGACCTTGTGATCTTAAGCTCTGTGGAGCTGAGTTCGTGATCAAAAGCATGA 71  
 Db 83 ValCysAspAspAspProIysSerIlePheSer-SerVal-----PheGluGluGluPr 100  
 QY 72 CGACAGCTGGCGGCC--GCGAATTCAGCTCTTTGACAGAGCTCAAGAGTGAAGAACTT 128  
 Db 100 oIleValLeuGluIulysHisIalaIasnGlyPheLeuCyAspAlaThrProValGlnSerVa 120  
 QY 129 AAACCCGAAGAAATTCAGATTCATGACACAGATCACAAAGTACTGTGGCTCGACTCTGG 188  
 Db 120 IAspCysIys-----LeuGlnAspIysAspGluIylValaIeValaIeValaGlyPr 137  
 QY 189 GAATTCATCAAGAGTCCAGAT-----AAAATCAATACAGCCCAAGATCTTCTTGC 242  
 Db 137 oHIGIulIeulValaIeulHisIeulLeuIylGlyAspIeulIysArgGluIValaIePheCy 157  
 QY 243 ATTAGCCTCATCCCTTGAAGCTCAGCCTCTGCGGAGAAAGAAAGTCCGATCTCTCGGGGCT 302  
 Db 157 sMetSerPheValaIeInGlyAspAspSerAspAspIys--IleProValThrLeuGlyIle 176

```

Oy      CCTCTAAAGGGAGGTTTGCTCTACTGT---GACCAAGATAAAGAACAAAGTCATCCATC 359
Db      176 elysolyllysasnlleuTYrlueSerCyValMetlyAsp-----AspThrProth 193
Oy      360 CCTTCAGCTGAGAAAGAGAACTGATGAAGCTGCTGCCCAAGAAAGATCAGCAGCCG 419
Db      193 rleuglnleu-----GluAspValAspProlySerTYrProlyeArgAspMetGluTy 211
Oy      420 GCCCTTCATCTTTATATAGGGCTCAGGTGGGCTCTCTGGAACATCTGAGATCGCGGCTCA 479
Db      211 sarGheValPheTYrLYrThrGluIleLysAsnArgValGluPheGlnSerAlaLeuTY 231
Oy      480 CCCCGATATGATTCATCTGCATCTGCACCTCTGCAATTGTAATGAAGCTCTGT 525
Db      231 rProantIrrPYrIleSerThrSerGlnAlaGluGlnLYrProVal 246

RESULT 8
S23010 interleukin-1 beta precursor - sheep
N|Alternate names: hematopoietin-1; IL-1 beta
C|Species: Ovis orientalis aries,Ovis ammon aries (domestic sheep)
C|Date: 08-Jun-1994 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004
C|Accession: S23010; S43047; S13092; B61246
R|Seew, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A|Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A|Reference number: S23010; MUID:92119335; PMID:1840515
A|Accession: S23010
A|Molecule type: mRNA
A|Residues: 1-266 <SEB>
A|Cross-references: UNIPROT:P21621; EMBL:X56972; NID:91808; PIDD:CAA40293.1; PID:91809
A|Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an additional
R|Sargan, D.R.
submitted to the EMBL Data Library, May 1992
A|Reference number: S43047
A|Accession: S43047
A|Molecule type: mRNA
A|Residues: 1-13,'C',15-54,'K',56-63,'A',65-144,'L',146-266 <SAR>
A|Cross-references: EMBL:X54796; NID:g1273; PIDD:CAA58566.1; PID:g1274
R|Fiskestrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A|Title: Nucleotide sequence of ovine interleukin-1 beta.
A|Reference number: S13092; MUID:91088326; PMID:2263490
A|Accession: S13092
A|Molecule type: mRNA
A|Residues: 1-13,'C',15-54,'K',56-61,'S',63,'A',65-144,'L',146-266 <FIS>
A|Cross-references: EMBL:X54796
A|Note: the authors translated the codon AGT for residue 62 as Arg
R|Andrews, A.R.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A|Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
A|Reference number: A61246; MUID:92120716; PMID:1769692
A|Accession: B61246
A|Molecule type: mRNA
A|Residues: 1-144,'L',146-266 <AND>
C|Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C|Comment: interleukin-1beta precursor is less heavily myristoylated than interleukin-1a)
C|Genetics:
A|Gene: IL-1-beta
C|Superfamily: interleukin-1
C|Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MA>

Alignment Scores:
Pred. No.: 4.13e-05 Length: 266
Score: 131.50 Matches: 44
Percent Similarity: 45.68% Conservative: 30
Best Local Similarity: 27.16% Mismatches: 63
Query Match: 11.60% Indels: 25
DB: 1 Gaps: 8

```

US-09-869-566-4 (1-650) x S23010 (1-266)

```

QY      58 TACAAAGAGATGACGACGCT-----GGCGCCCGCAATTACGCTTTTGACA 108
      103 PheGluThrSerSeraspGluLeuCyaspAlaIvalGlnSerValIysCysLys 122
QY      109 GGTCCAAAGATGAGAAGACTTAAACCCGAAGAAATTGAGATTCAGACCAAGATCAACAA 168
      123 -----LeuGlnAspArgGluGlnLys 129
QY      169 GACTGCTCTGAGCTCTGGG-----AATCTATGACAGCTTCAGATTAACAACTAC 219
      130 SerLeuValLeuAspSerProCysValLeuLysAlaLeuHisLeuProSerGlnGluMet 149
QY      220 ATACGCCAGAGATCTTTTTCATTAAGCTCATCTTCATGAGCTCACCTCTGGGAGAAA 279
      150 SerArg---GluValValPheCysMet---SerPheValGlnGlyGluGluArgAspAsn 167
QY      280 GGAAATCCGATTCCTCTGGGGGTCTCTAAAGGAGAGTTTGTCTTACTATGACAAAGAT 339
      168 LysIleProValAlaLeuGlyIleArgAspLysAsnLeuTyrLeuSerCysValLys--- 186
QY      340 AAAGACAAAGTCATCCATCCCTTCAGCTGAGAGAGAAAGAACTGATGAAGCTGGCTGCC 399
      187 LysGlyAspThr---ProThrLeuGlnLeu-----GluGluValAspProLysValTyr 203
QY      400 CAAAGAGATTCACAGACGGCGCCCTTCATCTTTTATAGGGCTCAGGTTGGGCTCTGGAAC 459
      204 ProLysArgAsnMetGluLysArgPheValPheTyrLysThrGluIleLysAsnThrVal 223
QY      460 ATGCTGAGAGTCGGCGGCTCACCCCGAGTGCATCTGCACTTCGCAATTGTAATGAG 519
      224 GluPheGluSerValLeuTyrProAsnTrpTyrIleSerThrSerGlnIleGluGluLys 243
QY      520 CCTGTT 525
      244 ProVal 245

```

# RESULT 9

JN0724  
Interleukin-1 beta precursor - pig  
N:Alternate names: hematopoietin-1; IL-1 beta  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 14-Jul-1994 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: JN0724  
R:Huether, M.J.; Lin, G.; Smith, D.M.; Murtough, M.P.; Molitor, T.W.  
Gene 129, 285-289, 1993  
A:Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 beta  
A:Reference number: JN0724; MUID:93314975; PMID:8325511  
A:Accession: JN0724  
A:Molecule type: mRNA  
A:Residues: 1-267 <HUE>  
A:Cross-references: UNIPROT:P26889; GB:M86725; NID:g164607; PIDN:AAA02584.1; PID:g164608  
A:Experimental source: alveolar macrophage  
C:Comment: This protein is a pleiotropic cytokine that mediates a variety of processes in  
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage  
ved form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.  
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a  
C:Superfamily: Interleukin-1  
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag  
F:115-267/Protein: interleukin-1 beta #status predicted <IL>  
F:77/Binding site: myristate (Lys) (covalent) #status predicted

## Alignment Scores:

Pred. No.: 0.000442 Length: 267  
Score: 121.50 Matches: 44  
Percent Similarity: 42.35% Conservative: 28  
Best Local Similarity: 25.88% Mismatches: 73  
Query Match: 10.71% Indels: 25  
DB: 1 Gaps: 7

US-09-869-566-4 (1-650) x JN0724 (1-267)

```

QY      64 GACGATGACGACGAC-----CTTGGC 84
      86 AspAspAspGlnLysSerIlePheSerPheIlePheGluGluProIleIleLeuGlu 105
QY      85 GCCCGGAATTACGCTCTTTTGGCAGAGTCCAAAGGTGMAAGATTAAACCCGAAGAAATTC 144
      106 ThrCysAsnAspAspPheValCysAspAlaAsnValGlnSerMetGluCysLys----- 123
QY      145 AGCATTCATGACCAAGATCAAAAGTACTGCTTCCTGAGCTCTGGGAAATCTCATACAGTT 204
      124 ---LeuGlnAspLysAspHisLysSerLeuValLeuAlaGlyProHisMetLeuLysAla 142
QY      205 CCAGAT-----AAAATCATACGCCAGAGATCTTTTTCATTAAGCTCATCTTTC 258
      143 LeuHisLeuLeuThrGlyAspLeuLysArgGluValAlaPheCysMet---SerPheVal 161
QY      259 ACCTACGCTCTGCGGAGAAAGAAAGTCCGATTCCTCTGGGGGTCTCTAAAGGAGATT 318
      162 GlnGlyAspAspSerAsnAsnLysIleProValThrLeuGlyIleLysGlyAsnLeu 181
QY      319 TGCTCTACTGT---GACAAAGATTAAGGACAAAGATCATCCCTTCAGCTGAAGAAAG 375
      182 TyrLeuSerCysValMetLysAsp-----AsnThrProThrLeuGlnLeu----- 196
QY      376 GAGAAACTGATGACAGCTGGCTGCCCAAAAGATACGACGCGGCTTCATCTTTTAT 435
      197 GluAspIleAspProLysArgTyrProLysArgAspMetGluLysArgPheValPheTyr 216
QY      436 AAGGCTCAGGTGGCTCTCTCGAAGCATGCTGAGTGGCGGCTCACCCCGAGATGTTCAATC 495
      217 LysThrGlnIleLysAsnArgValGluPheGluSerAlaLeuTyrProAsnTrpTyrIle 236
QY      496 TGCACCTCTGCATTTGTAATGAGCTGTT 525
      237 SerThrSerGlnAlaGluGlnLysProVal 246

```

## RESULT 10

I55969  
interleukin-1 beta precursor - mouse  
N:Alternate names: hematopoietin-1; IL-1 beta  
C:Species: Mus musculus (house mouse)  
C>Date: 26-Jul-1996 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: I55969; A24719; S13029  
R:Gray, P.W.; Gaisser, D.; Chen, E.; Goeddel, D.V.; Pennica, D.  
J. Immunol. 137, 3644-3648, 1986  
A:Title: Two interleukin-1 genes in the mouse: Cloning and expression of the cDNA for mu  
A:Reference number: I55969; MUID:87058957; PMID:3491144  
A:Accession: I55969  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-269 <RES>  
A:Cross-references: UNIPROT:P10749; GB:M15131; NID:g198293; PIDN:AAA39276.1; PID:g309398  
R:Reiford, J.L.; Machuga, G.; Massone, A.; Carinci, V.; Palla, E.; Meli, M.  
Nucleic Acids Res. 14, 9935-9963, 1986  
A:Title: The murine interleukin-1-beta gene: structure and evolution.  
A:Reference number: A24719; MUID:87117546; PMID:3492706  
A:Accession: A24719  
A:Molecule type: mRNA  
A:Residues: 1-269 <TEL>  
A:Cross-references: GB:X04964; NID:952666; PIDN:CAA28637.1; PID:g52667  
R:Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColi, A.S.; Geoghegan, K.F.; Otterness, I.C  
FEBS Lett. 278, 98-102, 1991  
A:Title: Reduction of biological activity of murine recombinant interleukin-1beta by sele  
A:Reference number: S13029; MUID:91130610; PMID:1993481  
A:Accession: S13029  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 118-269 <DAU>  
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage  
ved form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.  
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a  
C:Genetics:  
A:Gene: IL-1-beta



C/Superfamily: interleukin-1

C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen  
F/118-269/Product: interleukin-1 beta #status experimental <IL1>

Alignment Scores:

Pred. No.:	0.000561	Length:	269
Score:	120.50	Matches:	50
Percent Similarity:	46.67%	Conservative:	34
Best Local Similarity:	27.78%	Mismatches:	79
Query Match:	10.63%	Indels:	17
DB:	1	Gaps:	9

US-09-869-566-4 (1-650) x I55969 (1-269)

```

QY 49 GTTGTGCTGATCAAAAGCATGACGACAAAGCTTGGCGCGCAATTGACGCTTTGACAGA 108
DB 103 LeuCyAspSerTrpAspAspAsp-----AsnLeuValCysAsp 117
QY 109 GGTCCAAAGGTGAAAGCAATTAACCCGAAAGAAATTCAGATCAGCAGATCAAAA 168
DB 118 ValPro---IleArgIleuHis-----TyrArgLeuArgAspIleuGlnIly 133
QY 169 GACTGCTGCTG---GACTCTGGGAATCTCATAGCAGTTCA---GATAAACTACATA 222
DB 134 SerLeuValLeuSerAspProTyrGlnLeuValAlaLeuHisIleuAsnGlnIlyAsnIle 153
QY 223 CCGCCAGAAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282
DB 154 AsnGlnIleValIlePheSerMetSerPheValGlnGlnIlyGlnProSerAsnIly 172
QY 283 AGTCCGATCTCTCTGGGGGCTCTCTAAAGGGAAGTTTGTCTACCTGATGACAAAGATAA 342
DB 173 IleProValAlaLeuGlnIlyLeuValGlnIlyValSerValMetIlyAsp 192
QY 343 GGACAAAGTATTCATCCCTTTCAGCTGAAGAAAGAAAGAAAGTGAAGCTGGCTGCCAA 402
DB 193 GlyThr-----ProThrIleuGlnIleu-----GluSerValAspProIlyGlnIlyPro 208
QY 403 AAGGAATCAGCAGCGCGGCTTCATCTTTATAGGCTCAGGTGGGCTCTGGAACATG 462
DB 209 LysValLeuMetGlnIlyAspPheValPheAsnIlyIleGlnValIlySerValGln 228
QY 463 CTGAGAGTGGCGGCTCAGCCCGGATTCATCTGATGACCTCGCAATGTAATGAGCT 522
DB 229 PheGlnSerIleGlnIleProAsnTrpTyrIleSerThrSerGlnIleGlnIlySerPro 248
QY 523 GTTGGGTGACAGATTAATTTAGAACAGAAACACATGAAATTTTCATTTCAACCACT 582
DB 249 ValPheLeuGlnIlyAsnAsn---SerGlnIleAspIleIleAspPheThrMetGluSerVal 267

```

RESULT 11

ICBO1B

Interleukin-1 beta precursor - bovine

N/Alternate names: hematopoietin-1; IL-1 beta

C/Species: Bos primigenius taurus (cattle)

C/Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 09-Jul-2004

C/Accession: J10010; S01380

R/Mailiszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Mol. Immunol. 25, 429-437, 1988

A/Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin

A/Reference number: A9695; MUID:88318652; PMID:3261832

A/Accession: J10010

A/Molecule type: mRNA

A/Residues: 1-266 <MAL>

A/Cross-references: UNIPROT:P09428; GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201

R/Leong, S.R.; Flagers, G.M.; Lamm, M.; Gray, P.W. Nucleic Acids Res. 16, 9054, 1988

A/Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.

A/Reference number: S01380; MUID:89016591; PMID:3262866

A/Accession: S01380

A/Molecule type: mRNA

A/Residues: 1-251, 'A', 253-266 <LEO>

A/Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449

C/Comment: This protein is a cytokine that mediates a variety of immunoregulatory and inflammatory responses. This protein lacks a conventional signal sequence for protein export. Cleavage of form of interleukin-1 beta, unlike interleukin 1-alpha, is inactive.

C/Superfamily: interleukin-1

C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen  
F/114-266/Product: interleukin-1 beta #status predicted <MAT>

Alignment Scores:

Pred. No.:	0.00101	Length:	266
Score:	118.00	Matches:	46
Percent Similarity:	43.65%	Conservative:	33
Best Local Similarity:	25.41%	Mismatches:	76
Query Match:	10.41%	Indels:	26
DB:	1	Gaps:	8

US-09-869-566-4 (1-650) x ICBO1B (1-266)

```

QY 34 CTGTTGAGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 84
DB 74 LeuValGlnSerIleValIleValIleValIleValIleValIleValIleValIleVal 93
QY 85 -----GCCGCAATTCAGCTTTGACAGA 108
DB 94 PheIlePheGlnIleGlnIleProValIlePheGlnIlePheGlnIlePheGlnIlePheGlnIle 113
QY 109 GGTCCAAAGGTGAAAGCAATTAACCCGAAAGAAATTCAGATCAGCAGATCAAAA 168
DB 114 AlaPro---ValGlnSerIle-----LysCysValGlnGlnIleAspArgGlnIly 129
QY 169 GACTGCTGCTGAGCTGGGAATCTCATAGCAGTTCCAGAT-----AAAACTACATA 222
DB 130 SerLeuValLeuAlaSerProCysValIleValIleValIleValIleValIleValIle 149
QY 223 CCGCCAGAAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282
DB 150 AsnArgGlnValIleValPheCysMet---SerPheValGlnIlyGlnIlyValGlnIly 168
QY 283 AGTCCGATCTCTCTGGGGGCTCTCTAAAGGGAAGTTTGTCTACCTGATGACAAAGATAA 342
DB 169 IleProValAlaLeuGlnIlyIleLysAspIlyAsnLeuTyrLeuSerCysValIly 187
QY 343 GGACAAAGTATTCATCCCTTTCAGCTGAAGAAAGAAAGTGAAGCTGGCTGCCAA 402
DB 188 GlyAspThr---ProThrIleuGlnIleu-----GluGlnValAspProIlyValIlyPro 204
QY 403 AAGGAATCAGCAGCGCGGCTTCATCTTTATAGGCTCAGGTGGGCTCTGGAACATG 462
DB 205 LysValGlnMetGlnIlyAspPheValPheTyrIlySerThrSerGlnIleGlnIlySerPro 224
QY 463 CTGAGAGTGGCGGCTCAGCCCGGATTCATCTGATGACCTCGCAATGTAATGAGCT 522
DB 225 PheGlnSerIleGlnIleProAsnTrpTyrIleSerThrSerGlnIleGlnIlySerPro 244
QY 523 GTT 525
DB 245 Val 245

```

RESULT 12

ICBO1B

Interleukin-1 beta precursor (validated) - human

N/Alternate names: hematopoietin-1; IL-1 beta

C/Species: Homo sapiens (man)

C/Date: 28-Feb-1986 #sequence revision 15-May-1998 #text change 09-Jul-2004

C/Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S196

R/Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E. Nucleic Acids Res. 14, 7897-7914, 1986

A/Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev

A/Reference number: A25542; MUID:87040762; PMID:3490654

A/Accession: A25542

A/Molecule type: DNA; mRNA

A/Residues: 1-5, 'K', 7-269 <CLA>

A/Cross-references: UNIPROT:P01584; GB:X04500; NID:g33788

A>Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu  
 R.Beni, G.; Rangel, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.  
 Gene 52, 95-101, 1987  
 A>Title: Human interleukin-1 beta gene.  
 A:Reference number: A29019; MUID:87248099; PMID:2954882  
 A:Accession: A29019  
 A:Molecule type: DNA  
 A:Residues: 1-269 <BEN>  
 A:Cross-references: GB:M15840; NID:9186281; PIDN:AAA74137.1; PID:9386816  
 R.Auron, P.E.; Webb, A.C.; Rosemasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare  
 Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984  
 A>Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
 A:Reference number: A94023; MUID:85088517; PMID:6083565  
 A:Accession: A94023  
 A:Molecule type: mRNA  
 A:Residues: 1-5, 'K', 7-269 <AUR>  
 A:Cross-references: GB:K02770; NID:9186268; PIDN:AAA6106.1; PID:9307043  
 R.March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.  
 Nature 315, 641-647, 1985  
 A>Title: Cloning, sequence and expression of two distinct human interleukin-1 complement  
 A:Reference number: A93361; MUID:85240547; PMID:2989698  
 A:Accession: A93361  
 A:Molecule type: mRNA  
 A:Residues: 1-269 <MAR>  
 A:Cross-references: GB:X02532; NID:933789; PIDN:CAA26372.1; PID:933790  
 A>Note: parts of this sequence, including the amino end of the mature form, were confirm  
 R.Webb, A.C.; Dinarello, C.A.; Rosemasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au  
 Adv. Gene Technol. 22, 339-340, 1985  
 A>Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
 A:Reference number: 151852  
 A:Accession: 151852  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <WEB>  
 A:Cross-references: GB:M54933; NID:9186287; PIDN:AAA5136.1; PID:9186288  
 R.Nishida, T.; Nishino, N.; Takano, K.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hira  
 Biochem. Biophys. Res. Commun. 143, 345-352, 1987  
 A>Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.  
 A:Reference number: 152217; MUID:87156769; PMID:3493774  
 A:Accession: 152217  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-269 <NIS>  
 A:Cross-references: GB:M15330; NID:9186283; PIDN:AAA5135.1; PID:9307045  
 R.Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov,  
 I.I.; S.A.; Vinetkili, Y.P.  
 Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989  
 A>Title: Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin  
 A:Reference number: 138131; MUID:90249285; PMID:2635664  
 A:Accession: 138132  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-269 <ROT>  
 A:Cross-references: EMBL:X56087; NID:935662; PIDN:CAA9567.1; PID:935663  
 R.Csebo, K.M.; Wypych, J.; Yusechenko, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.  
 Blood 71, 962-968, 1988  
 A>Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic  
 A:Reference number: A90732; MUID:88184226; PMID:3381727  
 A:Accession: B27616  
 A:Molecule type: protein  
 A:Residues: 117-123, 'X', 125-126, 'X', 128 <ZSR>  
 R.Stevenson, F.T.; Burenson, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993  
 A>Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines  
 A:Reference number: A48293; MUID:93348250; PMID:8346241  
 A:Contents: annotation; myristylation of lysines  
 R.Handari, V.B.; Holmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.  
 Biochem. Biophys. Acta 1118, 25-35, 1991  
 A>Title: The role of arginine residues in interleukin 1 receptor binding.  
 A:Reference number: S19608; MUID:92110334; PMID:1837236  
 A:Contents: annotation; type 1 IL-1 receptor interaction site  
 A>Note: modification of Arg-120 by phenylglyoxal blocks receptor binding  
 R.Clore, G.M.; Gronenborn, A.M.

submitted to the Brookhaven Protein Data Bank, January 1991  
 A:Reference number: A50049; PDB:611B  
 A:Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269  
 R.Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.  
 Biochemistry 30, 2315-2323, 1991  
 A>Title: High-resolution three-dimensional structure of interleukin 1beta in solution by  
 A:Reference number: A44675; MUID:91159409; PMID:2001363  
 A:Contents: annotation; (1)H-NMR structural determination  
 R.Hazda, D.J.; Strickler, J.; Simon, P.; Young, P.R.  
 J. Biol. Chem. 266, 7081-7086, 1991  
 A>Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a conf  
 A:Reference number: A39774; MUID:91201363; PMID:2016316  
 A:Contents: annotation  
 R.Finzel, B.C.; Watenpau, K.D.; Einspa, H.M.  
 submitted to the Brookhaven Protein Data Bank, December 1989  
 A:Reference number: A50016; PDB:111B  
 R.Finzel, B.C.; Glancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpau, K.D.; Einspa, H.M.  
 J. Mol. Biol. 209, 779-791, 1989  
 A>Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolut  
 A:Reference number: A44666; MUID:90064532; PMID:2585509  
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage  
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 C:Superfamily: interleukin-1  
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage  
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 F:16/Binding site: myristate (Lys) (covalent) (partial) #status experimental  
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Alignment Scores:

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US-09-869-566-4 (1-650) x ICHU1B (1-269)

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus.n2p model

Run on: May 28, 2005, 17:32:11 ; Search time 72 Seconds  
(without alignments)  
6228.669 Million cell updates/sec

Title: US-09-869-566-4

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Searched: 1462099 segs, 344972447 residues  
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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result

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Query

SUMMARIES

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3	906	79.9	192	17	US-10-888-779-3	Sequence 3, Appli
4	906	79.9	192	17	US-10-888-867-3	Sequence 3, Appli
5	906	79.9	192	17	US-10-888-780-3	Sequence 3, Appli
6	906	79.9	192	17	US-10-888-931-3	Sequence 3, Appli
7	902	79.5	197	10	US-09-876-790-9	Sequence 9, Appli
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#### ALIGNMENTS

RESULT 1  
US-09-876-790-3  
; Sequence 3, Application US/09876790  
; Publication No. US20030091532A1  
GENERAL INFORMATION:  
APPLICANT: SIMS, John E.  
APPLICANT: SMITH, Dirk E.  
APPLICANT: BORN, Teresa L.  
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPICE VARIANTS AND XRE2 DNAS AND POLYPEPTID  
FILE REFERENCE: 2008-US  
CURRENT APPLICATION NUMBER: US/09/876,790  
PRIOR FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 60/112,163  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: 60/146,675  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: PCT/US99/29549  
PRIOR FILING DATE: 1999-12-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 192

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-876-790-3

## Alignment Scores:

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Query Match:	79.89%	Indels:	0
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US-09-869-566-4 (1-650) x US-09-876-790-3 (1-192)

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## RESULT 2

US-10-139-833-13  
Sequence 13, Application US/10139833  
Publication No. US20030004106A1  
GENERAL INFORMATION:  
APPLICANT: Satis, Christiaan M.  
APPLICANT: Giles, Jennifer  
APPLICANT: Mu, Sharon X.  
APPLICANT: Xia, Min  
APPLICANT: Babs, Michael B.  
APPLICANT: Cravello, Roger  
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and  
FILE REFERENCE: 00-1213-E  
CURRENT APPLICATION NUMBER: US/10/139,833  
CURRENT FILING DATE: 2002-05-06  
PRIOR APPLICATION NUMBER: 60/170,191  
PRIOR FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: 60/188,053  
PRIOR FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: 60/194,521  
PRIOR FILING DATE: 2000-04-04  
PRIOR APPLICATION NUMBER: 60/195,910

PRIOR FILING DATE: 2000-04-10  
PRIOR APPLICATION NUMBER: 09/724,583  
PRIOR FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13

## ALIGNMENT

US-09-869-566-4 (1-650) x US-10-139-833-13 (1-192)

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## RESULT 3

US-10-888-779-3  
Sequence 3, Application US/10888779  
Publication No. US20050009138A1  
GENERAL INFORMATION:  
APPLICANT: SIMS, John E.  
APPLICANT: SMITH, Dirk E.  
APPLICANT: BORN, Teresa L.  
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECE DNAS AND POLYPEPTII  
FILE REFERENCE: 2008-US  
CURRENT APPLICATION NUMBER: US/10/888,779  
CURRENT FILING DATE: 2004-07-09  
PRIOR APPLICATION NUMBER: US/09/876,790  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/112,163  
PRIOR FILING DATE: 1998-12-14

;; PRIOR APPLICATION NUMBER: 60/146,675  
;; PRIOR FILING DATE: 1999-11-10  
;; PRIOR APPLICATION NUMBER: PCT/US99/29549  
;; PRIOR FILING DATE: 1999-12-14  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 192  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-888-779-3

## Alignment Scores:

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DB 142 GlnSerAlaIaIaHisProGlyIyIyPheIleCyIyIySerCyAsnCyAsnGlnIyProVal 161  
QY 526 GGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCATTTCAACCACTTTC 585  
DB 162 GlyValIyIyIyAspIyPheGlyIyAsnArgIySHisIleGluPheSerPheGlnIyProVal 181  
QY 586 AAAGCTGAATAGAGCCCGAGTGAAGTCAAGAT 618  
DB 182 LysAlaGluMetSerProSerGlnValSerAsp 192

## RESULT 4

US-10-888-867-3  
;; Sequence 3, Application US/1088867  
;; Publication No. US2005009075A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SIMS, John E.  
;; APPLICANT: SMITH, Dirk E.  
;; APPLICANT: BORN, Teresa L.  
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND XRE2 DNAS AND POLYPEPTI  
;; FILE REFERENCE: 2008-US  
;; CURRENT APPLICATION NUMBER: US/10/888,867  
;; PRIOR FILING DATE: 2004-07-09  
;; PRIOR APPLICATION NUMBER: US/09/876,790  
;; PRIOR FILING DATE: 2001-06-06  
;; PRIOR APPLICATION NUMBER: 60/112,163

;; PRIOR FILING DATE: 1998-12-14  
;; PRIOR APPLICATION NUMBER: 60/146,675  
;; PRIOR FILING DATE: 1999-11-10  
;; PRIOR APPLICATION NUMBER: PCT/US99/29549  
;; PRIOR FILING DATE: 1999-12-14  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 192  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-888-867-3

## Alignment Scores:

Pred. No.:	2,51e-91	Length:	192
Score:	906.00	Matches:	171
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	17	Gaps:	0

US-09-869-566-4 (1-650) x US-10-888-867-3 (1-192)

QY 106 AAGGTCGCAAGGTGAAGAACTTAAACCGAAGAAATTCAGCATTCATGACGAGATCAC 165  
DB 22 ArgGlyProIyValIyAsnLeuAnProIySlyPheSerIlleHisAspGlnAspHis 41  
QY 166 AAGTACTGCTCTGAGCTCTGGGAATCTCATGACGATTCAGATTAATAAATCAATACGC 225  
DB 42 LysValIleValIleuAspSerGlyAsnLeuIlleAlaValProAspIyAsnIyrlleArg 61  
QY 226 CCAGAGATCTTCTTTCATTAAGCTCATCTTCAGCTCAGCTCGGAGAAAGAAAGT 285  
DB 62 ProGluIlePhePheIleuAlaSerSerIeSerIeSerIeAlaGluIySgIySer 81  
QY 286 CCGATTCCTCTGAGGATCTCTAAAGGAGATTGCTCTACTGTCAGCAAGATAAAGA 345  
DB 82 ProIleLeuLeuGlyValSerIySgIyIupheCyIeutyCyAspIyAspIySgIy 101  
QY 346 CAAAGTCATCCATCCCTTCAGCTGAAGAGAACTGATGAAGCTGCTGCCCAANG 405  
DB 102 GlnSerHisProSerIeIuIeulysGluIyLeuMetIySleuAlaIaGlnIyS 121  
QY 406 GAATGACAGCGCGGCTTCATCTTTTAAGGGCTCAGGTGGGCTCTGGAACATGCTG 465  
DB 122 GlnSerAlaIaArgProPheIlePheIyIyAlaGlnIyAlGlySerIyPheMetIeu 141  
QY 466 GAGTCGGCGGCTCACCCGAGATGTTTCATCTGACCTCTGCAATTGTAATGAGCTGTT 525  
DB 142 GlnSerAlaIaIaHisProGlyIyIyPheIleCyIyIySerCyAsnCyAsnGlnIyProVal 161  
QY 526 GGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCATTTCAACCACTTTC 585  
DB 162 GlyValIyIyIyAspIyPheGlyIyAsnArgIySHisIleGluPheSerPheGlnIyProVal 181  
QY 586 AAAGCTGAATAGAGCCCGAGTGAAGTCAAGAT 618  
DB 182 LysAlaGluMetSerProSerGlnValSerAsp 192

## RESULT 5

US-10-888-780-3  
;; Sequence 3, Application US/10888780  
;; Publication No. US20050013797A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SIMS, John E.  
;; APPLICANT: SMITH, Dirk E.  
;; APPLICANT: BORN, Teresa L.  
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND XRE2 DNAS AND POLYPEPTI  
;; FILE REFERENCE: 2008-US  
;; CURRENT APPLICATION NUMBER: US/10/888,780  
;; PRIOR FILING DATE: 2004-07-09  
;; PRIOR APPLICATION NUMBER: US/09/876,790  
;; PRIOR FILING DATE: 2001-06-06

/ PRIOR APPLICATION NUMBER: 60/112,163  
/ PRIOR FILING DATE: 1998-12-14  
/ PRIOR APPLICATION NUMBER: 60/146,675  
/ PRIOR FILING DATE: 1999-11-10  
/ PRIOR APPLICATION NUMBER: PCT/US99/29549  
/ PRIOR FILING DATE: 1999-12-14  
/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 3  
/ LENGTH: 192  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ US-10-888-780-3

## Alignment Scores:

Pred. No.:	2,51e-91	Length:	192
Score:	906.00	Matches:	171
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	17	Gaps:	0

US-09-869-566-4 (1-650) x US-10-888-780-3 (1-192)

QY 106 AAGGTCCTCAAGGTGAGAACTTAAACCGAAGAAATTCAGATTTCATGACAGATCAC 165  
DB 22 ArgGlyProLyValIysAsnLeuAnProLySlyPheSerIleHisAspGlnAspHis 41  
QY 166 AAGTCTGTGCTCTGAGCTCTGGGAATCTCATAGCAAGTTCAGATTAACATCAATCAACC 225  
DB 42 LysValIleValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnIlyrIleArg 61  
QY 226 CCAGAGATCTTCTTGATGATGAGCTCATGCTGAGCTCAGCTCGGAGAAAGAAAGT 285  
DB 62 ProGluIlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIleGluIlySer 81  
QY 286 CCGATTCTCTGCGGGGTCTCTAAAGGGAAGTTTGTCTCTACTGTGACAAGATAAGAA 345  
DB 82 ProIleLeuLeuGlyValSerIlyGlyIupheCySleuTyrcyAspLysAspIlysgly 101  
QY 346 CAAAGTCATCCATCCCTTGAGCTGAGAAAGAAAGAACTGATGAAGCTGCGCCCAAG 405  
DB 102 GlnSerHisProSerLeuGlnLeuIlySlySgIlySleuMetIlySleuAlaIleGlnIlyS 121  
QY 406 GAATCAGACGCGCGGCTTTCATCTTTATAGGGCTCAGGTGGGCTCCTGAAACATGCTG 465  
DB 122 GluSerAlaIlyArgProPheIlePheTyArgAlaGlnValGlySerIlyPheSmetIleu 141  
QY 466 GAGTCGGCGGCTCACCCCGAGATGTTTCATCTGACCTCTGCAATTTGATAGAGCTGTT 525  
DB 142 GluSerAlaIleHisProGlyTrpPheIleCySThrSerCyAsnCyAsnGlnProVal 161  
QY 526 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCAACCATTTGCG 585  
DB 162 GlyValIlyrAspLysPheGlnuAsnArgIlySHisIleGluPheSerPheGlnProValCyS 181  
QY 586 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCAT 618  
DB 182 LysAlaGluMetSerProSerGluValSerAsp 192

## RESULT 6

US-10-888-931-3  
/ Sequence 3, Application US/10888931  
/ Publication No. US20050013798A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SIMS, John E.  
/ APPLICANT: SMITH, Dirk E.  
/ APPLICANT: BORN, Teresa L.  
/ TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTI  
/ FILE REFERENCE: 2008-US  
/ CURRENT APPLICATION NUMBER: US/10/888,931  
/ CURRENT FILING DATE: 2004-07-09  
/ PRIOR APPLICATION NUMBER: US/09/876,790

/ PRIOR FILING DATE: 2001-06-06  
/ PRIOR APPLICATION NUMBER: 60/112,163  
/ PRIOR FILING DATE: 1998-12-14  
/ PRIOR APPLICATION NUMBER: 60/146,675  
/ PRIOR FILING DATE: 1999-11-10  
/ PRIOR APPLICATION NUMBER: PCT/US99/29549  
/ PRIOR FILING DATE: 1999-12-14  
/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 3  
/ LENGTH: 192  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ US-10-888-931-3

## Alignment Scores:

Pred. No.:	2,51e-91	Length:	192
Score:	906.00	Matches:	171
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	17	Gaps:	0

US-09-869-566-4 (1-650) x US-10-888-931-3 (1-192)

QY 106 AAGGTCCTCAAGGTGAGAACTTAAACCGAAGAAATTCAGATTTCATGACAGATCAC 165  
DB 22 ArgGlyProLyValIysAsnLeuAnProLySlyPheSerIleHisAspGlnAspHis 41  
QY 166 AAGTCTGTGCTCTGAGCTCTGGGAATCTCATAGCAAGTTCAGATTAACATCAATCAACC 225  
DB 42 LysValIleValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnIlyrIleArg 61  
QY 226 CCAGAGATCTTCTTGATGATGAGCTCATGCTGAGCTCAGCTCGGAGAAAGAAAGT 285  
DB 62 ProGluIlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIleGluIlySer 81  
QY 286 CCGATTCTCTGCGGGGTCTCTAAAGGGAAGTTTGTCTCTACTGTGACAAGATAAGAA 345  
DB 82 ProIleLeuLeuGlyValSerIlyGlyIupheCySleuTyrcyAspLysAspIlysgly 101  
QY 346 CAAAGTCATCCATCCCTTGAGCTGAGAAAGAAAGAACTGATGAAGCTGCGCCCAAG 405  
DB 102 GlnSerHisProSerLeuGlnLeuIlySlySgIlySleuMetIlySleuAlaIleGlnIlyS 121  
QY 406 GAATCAGACGCGCGGCTTTCATCTTTATAGGGCTCAGGTGGGCTCCTGAAACATGCTG 465  
DB 122 GluSerAlaIlyArgProPheIlePheTyArgAlaGlnValGlySerIlyPheSmetIleu 141  
QY 466 GAGTCGGCGGCTCACCCCGAGATGTTTCATCTGACCTCTGCAATTTGATAGAGCTGTT 525  
DB 142 GluSerAlaIleHisProGlyTrpPheIleCySThrSerCyAsnCyAsnGlnProVal 161  
QY 526 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCAACCATTTGCG 585  
DB 162 GlyValIlyrAspLysPheGlnuAsnArgIlySHisIleGluPheSerPheGlnProValCyS 181  
QY 586 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCAT 618  
DB 182 LysAlaGluMetSerProSerGluValSerAsp 192

## RESULT 7

US-09-876-790-9  
/ Sequence 9, Application US/09876790  
/ Publication No. US20030091532A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SIMS, John E.  
/ APPLICANT: SMITH, Dirk E.  
/ APPLICANT: BORN, Teresa L.  
/ TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTI  
/ FILE REFERENCE: 2008-US  
/ CURRENT APPLICATION NUMBER: US/09/876,790  
/ CURRENT FILING DATE: 2002-09-04



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1  PRIOR APPLICATION NUMBER: 60/112,163
2  PRIOR FILING DATE: 1998-12-14
3  PRIOR APPLICATION NUMBER: 60/146,675
4  PRIOR FILING DATE: 1999-11-10
5  PRIOR APPLICATION NUMBER: PCT/US99/29549
6  PRIOR FILING DATE: 1999-12-14
7  NUMBER OF SEQ ID NOS: 15
8
9  SOFTWARE: Patentin version 3.1
10
11  SEQ ID NO 9
12
13  LENGTH: 197
14
15  TYPE: PRT
16
17  ORGANISM: Homo sapiens
18
19  US-09-876-790-9

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Alignment Scores:	
Pred. No.:	7.04e-91
Score:	902.00
Percent Similarity:	93.62%
Best Local Similarity:	91.49%
Query Match:	79.54%
DB:	10
	1
Length:	197
Matches:	172
Conservative:	4
Mismatches:	6
Indels:	9
Gaps:	1

US-09-869-566-4 (1-650) x US-09-876-790-9 (1-197)

[illegible]

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RESULT 8
US-10-888-779--9
; Sequence 9, Application US/10888779
; Publication No. US20050009138A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPICE VARIANTS AND XREC2 DNAs AND POLYPEPTIDS

```

```

1 FILE REFERENCE: 2008-US
2
3 CURRENT APPLICATION NUMBER: US/10/888,779
4
5 CURRENT FILING DATE: 2004-07-09
6
7 PRIOR APPLICATION NUMBER: US/09/876,790
8
9 PRIOR FILING DATE: 2001-06-06
10
11 PRIOR APPLICATION NUMBER: 60/112,163
12
13 PRIOR FILING DATE: 1998-12-14
14
15 PRIOR APPLICATION NUMBER: 60/146,675
16
17 PRIOR FILING DATE: 1999-11-10
18
19 PRIOR APPLICATION NUMBER: PCT/US99/29549
20
21 PRIOR FILING DATE: 1999-12-14
22
23 NUMBER OF SEQ ID NOS: 15
24
25 SOFTWARE: PatentIn version 3.1
26
27 SEQ ID NO: 9
28
29 LENGTH: 197
30
31 TYPE: PRT
32
33 ORGANISM: Homo sapiens
34
35 US-10-888-779-9

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Alignment Scores:	
Pred. No.:	7,04e-91
Score:	902.00
Percent Similarity:	93.62%
Best Local Similarity:	91.49%
Query Match:	79,54%
DB:	17
Length:	197
Matches:	172
Conservative:	4
Mismatches:	6
Indels:	1
Gaps:	1

US-09-869-566-4 (1-650) x US-10-888-779-9 (1-1977)

[illegible]

RESULT 9  
US-10-888-867-9  
; Sequence 9, Application US/10888867  
; Publication No. US2005009075A1

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; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,867
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-888-867-9

Alignment Scores:
Pred. No.: 7.04e-91 Length: 197
Score: 902.00 Matches: 172
Percent Similarity: 93.62% Conservative: 4
Best Local Similarity: 91.49% Mismatches: 6
Query Match: 79.54% Indels: 6
DB: 17 Gaps: 1

US-09-869-566-4 (1-650) x US-10-888-867-9 (1-197)
QY 55 GACTACAAAGACGATGACGACAAAGCTTGCGCGCAATTGACGCTTTGGCAGAGTCCA 114
DB 16 AAPTTPGILuYsAspGluProGln-----CysCysLeuGluGluPro 29
QY 115 AAGGTGAAGAACTTAAACCCGAAAGAAATTGACGATTCATGACCAAGATCAAAAGTACTG 174
DB 30 LysValLysAsnLeuAsnProLysLysPheSerLLeHisAspGlnAspHisLysValLeu 49
QY 175 GTCTCGAGCTCTGGGAATCTCATGACAGTTCCAGATTAATAAATACTACGACCCAGAGATC 234
DB 50 ValLeuAspSerGlyAsnLeuLeaValProAspLysAsnTyrlLeArgProGluIle 69
QY 235 TTCTTTGCAATTAGCCTTCATCCTTGAGCTCAGCCTCGCGGAGAAAGAAAGATTC 294
DB 70 PhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLysGlySerProIleLeu 89
QY 295 CTGGGGGCTCTTAAAGGAGATTGTTCTCTACTGTGACAAAGATTAAGCAAAATGCAT 354
DB 90 LeuGlyValSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 109
QY 355 CCATCCCTTCAGCTGAAGAGAAAGAAAGAACTGAGCTGCGCCAAAGAAATCAGCA 414
DB 110 ProSerLeuGlnLeuLysLysGlyLysLeuMetLysLeuAlaAlaGlnLysGlnSerAla 129
QY 415 CGCGGCGCTTCATCTTTTATAGGGCTCAGGTGGGCTCTCTGAAACATGCTGAGTGGGG 474
DB 130 ArgArgProPheLLePheLysArgAlaGlnValGlySerLTrpAsnMetLeuGlnSerAla 149
QY 475 GCTCAACCCGAGATGTTCACTGACCTCTGCAATTGATGAGCTGTGGGGTGA 534
DB 150 AlaHisProGlyLTrpPheLLeCysThrSerCysAsnCysAsnGlnProValGlyValThr 169
QY 535 GATTAATTGAGAAACAGAAACACATTTGATTTTCAACCAAGTTTGCAGAGTGA 594
DB 170 AspLysPheGluAsnArgLysHisLLeGluPheSerPheGlnProValCysLysAlaGln 189
QY 595 ATGAGCCCAAGTGAAGTCAAGCAT 618
DB 190 MetSerProSerGlnValSerAsp 197
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RESULT 10
US-10-888-780-9
; Sequence 9, Application US/10888780
; Publication No. US20050013797A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTII
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,780
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-888-780-9

Alignment Scores:
Pred. No.: 7.04e-91 Length: 197
Score: 902.00 Matches: 172
Percent Similarity: 93.62% Conservative: 4
Best Local Similarity: 91.49% Mismatches: 6
Query Match: 79.54% Indels: 6
DB: 17 Gaps: 1

US-09-869-566-4 (1-650) x US-10-888-780-9 (1-197)
QY 55 GACTACAAAGACGATGACGACAAAGCTTGCGCGCAATTGACGCTTTGGCAGAGTCCA 114
DB 16 AAPTTPGILuYsAspGluProGln-----CysCysLeuGluGluPro 29
QY 115 AAGGTGAAGAACTTAAACCCGAAAGAAATTGACGATTCATGACCAAGATCAAAAGTACTG 174
DB 30 LysValLysAsnLeuAsnProLysLysPheSerLLeHisAspGlnAspHisLysValLeu 49
QY 175 GTCTCGAGCTCTGGGAATCTCATGACAGTTCCAGATTAATAAATACTACGACCCAGAGATC 234
DB 50 ValLeuAspSerGlyAsnLeuLeaValProAspLysAsnTyrlLeArgProGluIle 69
QY 235 TTCTTTGCAATTAGCCTTCATCCTTGAGCTCAGCCTCGCGGAGAAAGAAAGATTC 294
DB 70 PhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLysGlySerProIleLeu 89
QY 295 CTGGGGGCTCTTAAAGGAGATTGTTCTCTACTGTGACAAAGATTAAGCAAAATGCAT 354
DB 90 LeuGlyValSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 109
QY 355 CCATCCCTTCAGCTGAAGAGAAAGAAAGAACTGAGCTGCGCCAAAGAAATCAGCA 414
DB 110 ProSerLeuGlnLeuLysLysGlyLysLeuMetLysLeuAlaAlaGlnLysGlnSerAla 129
QY 415 CGCGGCGCTTCATCTTTTATAGGGCTCAGGTGGGCTCTCTGAAACATGCTGAGTGGGG 474
DB 130 ArgArgProPheLLePheLysArgAlaGlnValGlySerLTrpAsnMetLeuGlnSerAla 149
QY 475 GCTCAACCCGAGATGTTCACTGACCTCTGCAATTGATGAGCTGTGGGGTGA 534
DB 150 AlaHisProGlyLTrpPheLLeCysThrSerCysAsnCysAsnGlnProValGlyValThr 169
QY 535 GATTAATTGAGAAACAGAAACACATTTGATTTTCAACCAAGTTTGCAGAGTGA 594
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Db 170 AsblypBheglubnarglyshislllegluPheserPhelInProValCyslysaIaGlu 189  
Qy 595 ATAGAGCCCGAGTGGTACGCGAT 618  
Db 190 MetSerProSerGIuValSerasp 197

RESULT 11  
US-10-888-931-9  
; Sequence 9, Application US/10888931  
; Publication No. US20050013798A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECB DNAS AND POLYPEPT  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888, 931  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876, 790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 197  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-888-931-9

Alignment Scores:  
Pred. No.: 7,04e-91 Length: 197  
Score: 902.00 Matches: 172  
Percent Similarity: 93.62% Conservative: 4  
Best Local Similarity: 91.49% Mismatches: 6  
Query Match: 79,54% Indels: 6  
DB: 17 Gaps: 1

US-09-869-566-4 (1-650) x US-10-888-931-9 (1-197)  
Qy 55 GACTAAGAGATGATGACCAAGCTTGGCGCGCAATTGACCTCTTGGAGAGTCCA 114  
Db 16 AsbTPGluYaspluProGln-----CysCysleuGluGlyPro 29  
Qy 115 AAGTGAAGAACTTAACCGAAGAAATTGACGATTCATGACGAGATCAAGAACTACTG 174  
Db 30 lybVallybAsnleuasnProlysbysPheSerlleHiaspGlnasphlslybValleu 49  
Qy 175 GTCTGAGACTCTGGGATCTCATGACAGTTCCAGATTAATACTACATAGCCCGAGATC 234  
Db 50 ValLeuAspSerClyAsnleuIlealValProAspLybAsnTyrlleArgProGluIle 69  
Qy 235 TTCTTGGATTAAGCTCATCTTGGAGCTGACGCTTCGCGAAGAAAGAGTCCGATTC 294  
Db 70 PhePheAlaLeuAlaSerleuSerleuSerleuAlaSerleuAlaGluysGlySerProIleleu 89  
Qy 295 CTGGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGATTAAGGACAAAGTCA 354  
Db 90 LeuGlyValSerlysglyluPhecysleuTyrcysAspLybAspLybGlylnSerHls 109  
Qy 355 CCATCCCTTACGCTGAAGAGAGAAAGATGATGAAGCTGGCTGCCAAAAGAAATCAGA 414  
Db 110 ProSerleuGlnleuylsGlylsleuMetLybLeuAlaIlaGlnlysglylnSerAla 129  
Qy 415 CGCGGCGCTTATCTTTATAGGCTCAGGTGGGCTCTCTGAAACATGCTGAGAGTGGCG 474  
Db 130 ArgArgProPheIlePheTyrlArgAlaGlnValGlySerTyrlAsnMetleuGlnSerAla 149  
Qy 475 GCTCAACCCCGAGTGGTTCATCTGACCTCTCGCAATTGATGAGCCTGTGGGGGAGACA 534

Db 150 AlaHlsProGlyTrpPheIleCysThrSerCysAsnCyAsnIuProValGlyValThr 169  
Qy 535 GATTAATTTGAGAACGGAACACATTGAATTTTTCACACAGTGGTGAAGTGA 594  
Db 170 AsblypBheglubnarglyshislllegluPheserPhelInProValCyslysaIaGlu 189  
Qy 595 ATAGAGCCCGAGTGGTACGCGAT 618  
Db 190 MetSerProSerGIuValSerasp 197

RESULT 12  
US-09-788-963-6  
; Sequence 6, Application US/09788963  
; Patent No. US20020052473A1  
; GENERAL INFORMATION:  
; APPLICANT: YOUNG, PETER R.  
; APPLICANT: MCDONNELL, PETER C.  
; APPLICANT: KUMAR, SANJAY  
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4  
; FILE REFERENCE: GP-70607-1C1  
; CURRENT APPLICATION NUMBER: US/09/788, 963  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 09/293, 625  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 09/452,140  
; PRIOR FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-788-963-6

Alignment Scores:  
Pred. No.: 4,22e-90 Length: 198  
Score: 895.00 Matches: 169  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 78,92% Indels: 0  
DB: 9 Gaps: 0

US-09-869-566-4 (1-650) x US-09-788-963-6 (1-198)  
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Db 30 ProlybVallybAsnleuasnProlysbysPheSerlleHiaspGlnasphlslybVal 49  
Qy 172 CTGCTCTGAGACTCTGGGATTCATGACAGTTCCAGATTAATACTACATAGCCGAG 231  
Db 50 LeuValleuAspSerClyAsnleuIlealValProAspLybAsnTyrlleArgProGlu 69  
Qy 232 ATCTTCTTGGATTAAGCTCATCTTGGAGCTGACGCTTCGCGAAGAAAGAGTCCGAT 291  
Db 70 IlePhePheAlaLeuAlaSerleuSerleuSerleuAlaSerleuAlaGluysGlySerProIle 89  
Qy 292 CTCTGGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGATTAAGGACAAAG 351  
Db 90 LeuLeuGlyValSerlysglyluPhecysleuTyrcysAspLybAspLybGlylnSer 109  
Qy 352 CATTCATCCCTTACGCTGAAGAGAGAAAGATGATGAAGCTGGCTGCCAAAAGAAAT 411  
Db 110 HlsProSerleuGlnleuylsGlylsleuMetLybLeuAlaIlaGlnlysglylnSer 129  
Qy 412 GCAGCGCGGCTTATCTTTATAGGCTCAGGTGGGCTCTCTGAAACATGCTGAGAGTGG 471  
Db 130 AlaArgArgProPheIlePheTyrlArgAlaGlnValGlySerTyrlAsnMetleuGlnSer 149  
Qy 472 GCGGCTCAACCCCGAGTGGTTCATCTGACCTCTCGCAATTGATGAGCCTGTGGGGTG 531  
Db 150 AlaAlaHlsProGlyTrpPheIleCysThrSerCysAsnCyAsnGluProValGlyVal 169

QY 532 ACAGATAATTTGAGACGAGAAACATTTGATTTTCACACGATTTGCAAGCT 591  
DB 170 TTTAspLysPheGluAsnArgLysHisIleGluPheSerPheGluProValCysLysAla 189  
QY 592 GAAATGAGCCCACTGAGTCCGAT 618  
DB 190 GluMetSerProSerGluValSerAsp 198

RESULT 13  
US-09-788-963-2  
; Sequence 2, Application US/09788963  
; Patent No. US20020052473A1  
; GENERAL INFORMATION:  
; APPLICANT: YOUNG, PETER R.  
; APPLICANT: McDONNELL, PETER C.  
; APPLICANT: KUMAR, SANJAY  
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4  
; FILE REFERENCE: GP-70507-1C1  
; CURRENT APPLICATION NUMBER: US/09/788,963  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 09/293,625  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 09/452,140  
; PRIOR FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-788-963-2

Alignment Scores:

Pred. No.:	4,356-90	Length:	218
Score:	895.00	Matches:	169
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.92%	Indels:	0
DB:	9	Gaps:	0

US-09-869-566-4 (1-650) x US-09-788-963-2 (1-218)

QY 112 CCAAGGTGAGAACTTTAAACCCGAAAGAAATTCAGATTCATGACGATCACAAGTA 171  
DB 50 ProlYsValLysAsnLeuAsnProLysPheSerIleHisAspGlnAspHisLysVal 69  
QY 172 CTGCTCTCGAAGCTCTGGAATCTCATAGCAAGTCCAGATAAAACATCACTAGCCGAG 231  
DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrIleArgProGlu 89  
QY 232 ATCTTCTTGATTAAGCTCATCTGAGCTCAGCTTCGCGAGAAAGAAATGCCGATT 291  
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QY 292 CTCCTCGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTCGACAGATTAAGCAAGT 351  
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QY 352 CATTCATCCCTTCAGCTGAGAAAGAGAAAGAACTGATGAGCTGCGCAAAAAGAAATCA 411  
DB 130 HisProSerLeuGlnLeuLysLysGlyLysLeuMetLysLeuAlaIleGlnLysGlnSer 149  
QY 412 GCAGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCTGGAACAATGCTGAGTGC 471  
DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTyrAsnMetLeuGlnSer 169  
QY 472 GCGGCTACCCCGAGATGTTGATCTGACCTCTGCAATTTGATAGAGCTGTGGGGTG 531  
DB 170 AlaAlaHisProGlyTyrPheIleCysThrSerCysAsnGlnProValGlyVal 189  
QY 532 ACAGATAATTTGAGAAACGAGAAACATTTGATTTTCATTTCAACGATTTGCAAGCT 591  
DB 190 TTTAspLysPheGluAsnArgLysHisIleGluPheSerPheGluProValCysLysAla 209

QY 592 GAAATGAGCCCACTGAGTCCGAT 618  
DB 210 GluMetSerProSerGluValSerAsp 218

RESULT 14  
US-09-876-790-8  
; Sequence 8, Application US/09876790  
; Publication No. US20030091532A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John B.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa U.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 8  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-876-790-8

Alignment Scores:

Pred. No.:	4,356-90	Length:	218
Score:	895.00	Matches:	169
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.92%	Indels:	0
DB:	10	Gaps:	0

US-09-869-566-4 (1-650) x US-09-876-790-8 (1-218)

QY 112 CCAAGGTGAGAACTTTAAACCCGAAAGAAATTCAGATTCATGACGATCACAAGTA 171  
DB 50 ProlYsValLysAsnLeuAsnProLysPheSerIleHisAspGlnAspHisLysVal 69  
QY 172 CTGCTCTCGAAGCTCTGGAATCTCATAGCAAGTCCAGATAAAACATCACTAGCCGAG 231  
DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrIleArgProGlu 89  
QY 232 ATCTTCTTGATTAAGCTCATCTGAGCTCAGCTTCGCGAGAAAGAAATGCCGATT 291  
DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLysGlySerProIle 109  
QY 292 CTCCTCGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTCGACAGATTAAGCAAGT 351  
DB 110 LeuLeuGlyValSerLysGlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSer 129  
QY 352 CATTCATCCCTTCAGCTGAGAAAGAGAAAGAACTGATGAGCTGCGCAAAAAGAAATCA 411  
DB 130 HisProSerLeuGlnLeuLysLysGlyLysLeuMetLysLeuAlaIleGlnLysGlnSer 149  
QY 412 GCAGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCTGGAACAATGCTGAGTGC 471  
DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTyrAsnMetLeuGlnSer 169  
QY 472 GCGGCTACCCCGAGATGTTGATCTGACCTCTGCAATTTGATAGAGCTGTGGGGTG 531  
DB 170 AlaAlaHisProGlyTyrPheIleCysThrSerCysAsnGlnProValGlyVal 189  
QY 532 ACAGATAATTTGAGAAACGAGAAACATTTGATTTTCATTTCAACGATTTGCAAGCT 591  
DB 190 TTTAspLysPheGluAsnArgLysHisIleGluPheSerPheGluProValCysLysAla 209



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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus.rnp model

Run on: May 28, 2005, 16:28:55 ; Search time 95.5 Seconds  
(without alignments)  
6970.711 Million cell updates/sec

Title: US-09-869-566-4  
Perfect score: 1134  
Sequence: 1 tcaatcaccatgctgcact.....cgactctagagatcccg99 650

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 segs, 512079187 residues  
Total number of hits satisfying chosen parameters: 3224756

Minimum DB seg length: 0  
Maximum DB seg length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ rnp model -DEV=rlp  
-Q=/cgn2.1/USPTO.epool.p/US09869566/runat\_27052005\_163130\_19910/app\_query.faeta.1.839  
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-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09869566 @CGN 1.1 152 @runat\_27052005\_163130\_19910 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEBUFFER -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONELOG  
-BEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	895	78.9	218	1	II1F7_HUMAN	Q9nzh6 homo sapien
2	848	74.8	219	2	Q7RU00	Q7RU00 homo sapien
3	229.5	20.2	169	1	II1F9_HUMAN	Q9nzh8 homo sapien
4	229.5	20.2	169	2	Q7RTZ9	Q7RTZ9 homo sapien
5	229	20.2	157	2	Q7RTZ7	Q7RTZ7 homo sapien
6	212	18.7	158	1	II1F6_HUMAN	Q9nzh7 homo sapien
7	212	18.7	158	2	Q7RTZ8	Q7RTZ8 homo sapien
8	199	17.5	183	1	II1F5_MOUSE	Q9d4z6 mus musculi
9	191.5	16.9	156	1	II1F5_MOUSE	Q9d4z6 mus musculi
10	190	16.8	134	2	Q6UVX7	Q6UVX7 homo sapien
11	174.5	15.4	155	1	II1F5_HUMAN	Q9nzh0 h interleuk
12	174.5	15.4	155	2	Q7RTZ6	Q7RTZ6 homo sapien
13	174.5	15.4	164	1	II1F9_MOUSE	Q8r4t0 mus musculi
14	173	15.3	159	2	Q8CGA1	Q8CGA1 mus musculi
15	171	15.1	160	1	II1F6_MOUSE	Q9j1a2 mus musculi
16	167	14.7	178	1	II1X_MOUSE	P25085 mus musculi

17	165.5	14.6	152	1	II1FA_MOUSE	Q8r459 mus musculi
18	158.5	14.0	159	2	Q7RTZ4	Q7RTZ4 homo sapien
19	158.5	14.0	177	1	II1X_HUMAN	P18510 homo sapien
20	156.5	13.8	152	1	II1FA_HUMAN	Q8wz1 h interleuk
21	156.5	13.8	152	2	Q7RTZ5	Q7RTZ5 homo sapien
22	156.5	13.8	267	2	Q73909	Q73909 gallus galli
23	154.5	13.6	177	1	II1X_RABIT	P26890 oryctolagus
24	152	13.4	174	1	II1X_BOVIN	Q77482 bos taurus
25	151	13.3	176	1	II1X_CANFA	Q9bnd0 canis fami
26	150	13.2	177	1	II1X_TURTR	Q9gm4 turrisops tr
27	149	13.1	272	2	Q9DDF2	Q9ddf2 cyprinus ca
28	148	12.9	177	1	Q866R8	Q866R8 macaca fasc
29	146.5	12.9	177	2	II1X_PIG	Q29056 sus scrofa
30	146.5	12.8	178	1	II1X_RAT	P25086 ratus norv
31	145.5	12.8	272	2	Q8AXV9	Q8axv9 carassius a
32	139.5	12.3	272	2	Q712J8	Q712J8 carassius a
33	137.5	12.1	177	1	II1X_HORSE	Q18999 equus cabal
34	137.5	12.1	272	2	Q9DDF3	Q9ddf3 cyprinus ca
35	136	12.0	273	2	Q7T056	Q7t056 brachydanto
36	135.5	11.9	267	2	Q29082	Q29082 sus scrofa
37	132.5	11.7	211	2	Q7YS41	Q7ys41 sus scrofa
38	131.5	11.6	266	1	II1B_SHEEP	P21621 ovib aries
39	129.5	11.4	276	2	Q57398	Q57398 cyprinus ca
40	129.5	11.4	276	2	Q9PW18	Q9pw18 cyprinus ca
41	128.5	11.3	238	2	Q8AXV8	Q8axv8 carassius a
42	127.5	11.2	82	2	Q6PUJ3	Q6puj3 sus scrofa
43	121.5	10.7	267	1	II1B_PIG	P26893 sus scrofa
44	121	10.7	268	1	II1B_RAT	Q63264 ratus norv
45	120.5	10.6	269	1	II1B_MOUSE	P10749 mus musculi

## ALIGNMENTS

RESULT 1  
II1F7\_HUMAN STANDARD; PRT; 218 AA.  
ID Q9NZH6; Q8TFD04; Q8TD05; Q9HBF2; Q9HBF3; Q9UHA6;  
AC Q9NZH6; Q8TFD04; Q8TD05; Q9HBF2; Q9HBF3; Q9UHA6;  
AD 28-FEB-2003 (Rel. 41) Created  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Interleukin 1 family member 7 precursor (II1F7) (interleukin-1 zeta)  
DE (II1F7 zeta) (Fili zeta) (interleukin-1 homologue 4) (II1F4)  
DE (interleukin-1-related protein) (II1RPI) (II1X protein).  
GN Name=II1F7; Synonyms=FIILZ, IL1H4, IL1RPI;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RC TISSUE=Fetal B-cell, Fetal colon, Fetal lung, and Fetal testis;  
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;  
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
RA Griswold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L.,  
RA Young P.R.;  
RT "Identification and initial characterization of four novel members of  
RT the interleukin-1 family.";  
RT J. Biol. Chem. 275:10308-10314(2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RC TISSUE=Colon carcinoma;  
RX Manoj P.P., Mantovani A., Muzio M.;  
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS B AND C), SEQUENCE OF 46-54, AND VARIANTS  
RP VAL-31 AND ALA-42.  
RX MEDLINE=21066552; PubMed=1145836; DOI=10.1006/cyto.2000.0799;  
RA Pan G., Riser P., Mo W., Baldwin D.T., Zhong A.W., Pilvaroff E.,  
RA Yaneura D., Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R.,  
RT IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-  
RT IL1R-";  
RN Cytokine 13:1-7(2001).  
RN [4]

RP SEQUENCE FROM N.A. (ISOFORM A).  
 RX MEDLINE:20092888; PubMed:10625660; DOI=10.1074/jbc.275.2.1169;  
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Rubin M., Garika K.E.,  
 RA Sims J.E.;  
 RT "Four new members expand the IL-1 superfamily.";  
 RL J. Biol. Chem. 275:1169-1173(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS D AND E).  
 RX MEDLINE:2198051; PubMed:1191773; DOI=10.1006/geno.2002.6752;  
 RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;  
 RT "Genomic organization of the interleukin-1 locus.";  
 RL Genomics 79:726-733(2002).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS VAL-31 AND ATA-42.  
 RC TISSUE=Placenta;  
 RX MEDLINE:23188257; PubMed:12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Murthy D.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Bottrighe A.S., Krzywinski M.I., Skalska D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Binds to Interleukin-18 receptor (IL-18R) receptor but  
 not to IL-1 receptor. Could be a new player in the inflammatory  
 and immune responses mediated by the IL-18/IL-18R axis.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=5;  
 CC Name=B;  
 CC IsoId=Q9NZH6-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=Q9NZH6-2; Sequence=VSP\_002653;  
 CC Name=C;  
 CC IsoId=Q9NZH6-3; Sequence=VSP\_002656;  
 CC Name=D;  
 CC IsoId=Q9NZH6-4; Sequence=VSP\_002654;  
 CC Name=E;  
 CC IsoId=Q9NZH6-5; Sequence=VSP\_002655;  
 CC -1- TISSUE SPECIFICITY: Isoforms A, B and C are expressed in testis,  
 colon, placenta, lung and lymph node. Isoforms D and E were found  
 only in testis and bone marrow. Whereas only isoform A is found in  
 brain, only isoform B in kidney and only isoform C in heart.  
 CC -1- INDUCTION: By phorbol ester (PMA) in different cell lines.  
 CC -1- SIMILARITY: Belongs to the IL-1 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; AF200496; AAF69252.1; -;  
 DR EMBL; AF167368; AAG29344.1; -;  
 DR EMBL; AF251118; AAG14420.1; -;  
 DR EMBL; AF251120; AAG14422.1; -;  
 DR EMBL; AF251119; AAG14421.1; -;  
 DR EMBL; AF201832; AAF25212.1; -;

DR EMBL; AY071840; AAL67151.1; -;  
 DR EMBL; AY071841; AAL67154.1; -;  
 DR EMBL; BC020637; AAH20637.1; -;  
 DR HSSP; P18510; IL1R.  
 DR Genew; HGNC:15563; IL1F7.  
 DR H-INVD; HIX0002387; -;  
 DR MIM; 605510; -;  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR008996; CytoK IL1 like.  
 DR InterPro; IPR00975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR PRINTS; PR00264; INTERLEUKIN1.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM0125; IL1; 1.  
 DR SMART; PS00253; INTERLEUKIN\_1; FALSE\_NEG.  
 DR Alternative splicing; CytoKine; Direct protein sequencing;  
 KW Multigene family; Polymorphism.  
 FT PROPEP 1 45  
 FT CHAIN 46 218  
 FT VARSPLIC 1 49  
 FT VARSPLIC 28 49  
 FT VARSPLIC 28 88  
 FT VARSPLIC 49 89  
 FT VARIANT 31 31  
 FT VARIANT 42 42  
 FT SEQUENCE 218 AA; 24126 MW; 96B089310D2CEA68 CRC64;  
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 Score: 895.00 Matches: 169  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 78.92% Indels: 0  
 DB: 1 Gaps: 0  
 US-09-869-566-4 (1-650) x 11F7\_HUMAN (1-218)  
 QY 112 CCAAAAGTGAGAACTTAAACCCGAAAGAAATTCAGATTATGACCGAGATCAAAAGTA 171  
 DB 50 ProlysVallyAlaAsnLeuAsnProlyslsPhseSerIleHisAspClnAspHislyVal 69  
 QY 172 CTGGTCTGAGACTCTGGGGAATCTCATAGAGATTCAGATTAAGTACCTAGCCCAAG 231  
 DB 70 LeuValLeuAspSerClyAsnLeuIleAlaValProAspLyAsAsnIlyrIleArgProGlu 89  
 QY 232 ATCTTCTTGATTCATTCGCTTCATCTGAGCTGAGCTGCGGAGAAAGAAATTCGATT 291  
 DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluysGlySerProIle 109  
 QY 292 CTCCTGGGGGCTCTTAAAGGGAGATTTCCTCTACTGAGCAAGATTAAGACAAAGT 351  
 DB 110 LeuLeuGlyValSerIlyslgIuPheCysLeuIlyrCyAspLyAspLyAspLyGlyGlnSer 129  
 QY 352 CATTCATCCCTTCAGCTGAAGAGAACTGATGAGAGCTGGCTGCCCAAAAGAAATTA 411  
 DB 130 HisProSerLeuGlnLeuIlyslgIuysLeuMetLySLeuAlaAlaGlnIlysgIuSer 149  
 QY 412 GCAAGCGCGGCGCTTATATAGGGCTGAGTGGCTCTCGAACAATGCTGAGAGTGC 471  
 DB 150 AlaArgArgProPheIlePheIlyrArgAlaGlnValGlySerIlyrPasnMetLeuGlnSer 169



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QY 472 GCGGCTCACCAGGATGTCATCTGACCTCTCGCATTTGATAGAGCTGTGGGGTG 531
DB 170 AAlAlHisProGlyTrpPheIleCythrSerCysAsnGluPValGlyVal 189
QY 532 ACGATTAATTTGAGAACGAGAAACATTTGATTTTCACTTGAAGT 591
DB 190 ThAspLysPheGluAsnArgLysHsIleGluPheSerPheGlnProValCysLysAla 209
QY 592 GAAATGAGCCCGAGTGGGTGACGAGT 618
DB 210 GluMetSerProSerGluValSerAsp 218

RESULT 2
Q7RU00 PRELIMINARY; PRT; 219 AA.
AC Q7RU00;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IL-1F7b (IL-1H4, IL-1H, IL-1RPL).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545212; PubMed=11093146;
RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
RT Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RT Eur. J. Immunol. 30:3299-3308(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;
RA Gotingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,
RA Hildebrand F.;
RA "Molecular cloning of the interleukin-1 gene cluster: construction of
RT an integrated YAC/PAC contig and a partial transcriptional map in the
RT region of chromosome 2q13.";
RT Genomics 41:370-378(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245215; PubMed=8188271;
RA Nicklin M.J.H., Weith A., Duff G.W.;
RA "A physical map of the region encompassing the human interleukin-1
RT alpha, interleukin-1-beta and interleukin-1 receptor genes.";
RT Genomics 19:382-384(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21888050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
RA Korman K.;
RA "A sequence-based map of the nine genes of the human interleukin-1
RT cluster.";
RT Genomics 79:718-725(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/birc.1999.1440;
RA Mulero J.U., Pace A.M., Nelken S.T., Loeb D.D., Correa T.R.,
RA Drmanac R., Ford J.E.;
RA "IL1H4: A novel interleukin-1 receptor antagonist gene.";
RA Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Rubin M., Garza K.E.,
RA Sims J.E.;
RA "Four new members expand the interleukin-1 superfamily.";
RA J. Biol. Chem. 275:1169-1175(2000).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RA "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RT J. Biol. Chem. 275:10308-10314(2000).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
RA "Identification and gene organization of three novel members of the
RT IL-1 family on human chromosome 2.";
RT Genomics 66:213-216(2000).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
RA Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Puise J.,
RA Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
RT "Cloning and characterization of IL-1HY2, a novel interleukin-1 family
RT member.";
RT J. Biol. Chem. 276:20597-20602(2001).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359532; PubMed=1146363;
RA Debeets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
RA Kastelein R.A.;
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
RT as an antagonist and agonist of NF-kB activation through the orphan
RT IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.";
RT J. Immunol. 167:1440-1446(2001).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3;
RA Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,
RA Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.U., Pan G.,
RA Pan Y., Smith D.E., Young P.R.;
RT "A new nomenclature for the IL-1-family genes.";
RT Trends Immunol. 22:536-537(2001).
CC -I- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBD third party annotation (TFA) entry.
CC -I- SIMILARITY: Belongs to the IL-1 family.
DR EMBL; BN000002; CAD29873.1; -.
DR HSSP; O9OY1; IMD6.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005152; P:interleukin-1 receptor antagonist activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok_IL1_Like.
DR InterPro; IPR003297; InterleukinIL1RA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PRO0264; INTERLEUKIN1.
DR PRINTS; PRO1360; INTERLEUKIN1X.
DR ProDom; PD002536; Interleukin_1; 1.
SQ SEQUENCE 219 AA; 24242 MW; 18EBA081DF25C41 CRC64;

Alignment Scores:
Pred. No.: 1,66e-76 Length: 219
Score: 848.00 Matches: 171
Percent Similarity: 86.76% Conservatave: 6
Best Local Similarity: 83.82% Mismatches: 11
Query Match: 74.78% Indels: 16
DB: Gaps: 3

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US-09-869-566-4 (1-650) x Q7RU00 (1-219)
QY 55 GACTACAAAGACATGACGACAAAGCTTGGG-----GCCGCGAATTCAAGCTCTTGGC 105
Db 16 AaPTTgPILuYasPpILuProGInCysCysLeuGluAsPProhlaIaIySerProLeuGlu 35
QY 106 AGAGTCCA-----AAGTGAAGAACTTA 129
Db 36 ProGILyPProSerLeuProTherMetAanPheValHleThSerArgyVallySerLeu 55
QY 130 AACCCGAAGAAATTCGCAATTCATGACCGAGATCAAGAAAGTACTGCTCGACTCTGGG 189
Db 56 AaPProLYaLysPheSerIleHleSaPGLInAsPHeLysValLeuValLeuAsPSeRgLy 75
QY 190 AATCTCATGACAGTTCCAGATTAAGAACTACATACGCCGAGAGATCTCTTGGCATTAAGCC 249
Db 76 AaHleuIleHlaValaProaAsPlySaenTyIleArgPProGILuIlePheHleAlaLeuAla 95
QY 250 TCATCCTTGAGCTCAGCCTCTCTGCGAAGAAAGAGTCCGATTCCTCGGGGCTCTTA 309
Db 96 SerSerLeuSerSerLeuSerAlaSerAlaGluLySGLySerLeuIleLeuLeuGlyValSerLy 115
QY 310 GGGGAGTTTGTCTTCTACTGTGACAGATTAAGCAAGATGATCTCATTCCTTCAGCTG 369
Db 116 GLyGluPhaCysLeuTyrcysAsPlySaPlySGLyGlnSerHisProSerLeuGlnLeu 135
QY 370 AAGAAGAGAAATCTGATGAAGCTGGCGCCCAAGAAAGATCAAGCCGCGCTTCATC 429
Db 136 LysLysGlnLysLeuLeuLysLeuAlaAlaGlnLysGlnSerAlaArgArgProPheIle 155
QY 430 TTTTATAGGCTCAGTGGGCTCTCTGGAACATGCTGAGTGGCGGCTCAACCCGGATG 489
Db 156 PheTyArgAlaGlnValGlySerArgaAaMetLeuGlnSerAlaAlaHisProGlyTyr 175
QY 490 TTCATTCGACCTCCCTCGCAATTTGTAATGAGCCTGTGGGGTGACAGATTAATTGGAAC 549
Db 176 PheIleCysThrSerCysaSnCysaSnGlnProValGlyValThraPlySaPheGluAa 195
QY 550 AGGAACACATTAATTTTCATTTCAACCA---GTTTGAAAGCTGAATGAGCCCGAGT 606
Db 196 ArgLysHleIleGlnLysSerPheGlnProValValCysLysAlaGlnLysSerProSer 215
QY 607 GAGGTGAGCAT 618
Db 216 GluValSerAsn 219

RESULT 3
ID 11F9_HUMAN STANDARD; PRT; 169 AA.
AC Q9NZH8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin 1 family member 9 (IL-1F9) (Interleukin-1 homolog 1) (IL-1H1) (Interleukin-1 epsilon) (IL-1 epsilon) (IL-1 related protein 2) (IL-1RP2).
GN Name=IL1F9; Synonyms=IL1E, IL1H1, IL1RP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Keratinocytes;
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [2]

```

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RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Epithelium;
RX MEDLINE=21359532; PubMed=11466363;
RA Debats R., Timane J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
RA Kastelein R.A.;
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
RT as an antagonist and agonist of NF-kappa B activation through the
RT orphan IL-1 receptor-related protein 2.";
RL J. Immunol. 167:1440-1446(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
RA Bustfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
RT "Identification and gene organization of three novel members of the
RT IL-1 family on human chromosome 2.";
RL Genomics 66:213-216(2000).
CC -I- FUNCTION: Function as an agonist of NF-kappa B activation through
CC the orphan IL-1-receptor-related protein 2. Could constitute part
CC of an independent signaling system analogous to interleukin-1
CC alpha (IL-1A), beta (IL-1B) receptor agonist and interleukin-1
CC receptor type 1 (IL-1R1), that is present in epithelial barriers
CC and takes part in local inflammatory response.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Highly expressed in tissues containing
CC epithelial cells: skin, lung, stomach and esophagus. In skin is
CC expressed only in keratinocytes but not in fibroblasts,
CC endothelial cells or melanocytes. Up-regulated in lesional
CC psoriasis skin.
CC -I- INDUCTION: By TNF-alpha and by IFN-gamma in keratinocytes.
CC -I- SIMILARITY: Belongs to the IL-1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL: AF200492; AAF69248.1; -.
DR EMBL: AF206696; AAG35670.1; -.
DR HSSP: P18510; IL1R.
DR Genew; HGNC:15741; IL1F9.
DR MIM: 605542; -.
DR GO: GO:0007267; P:cell-cell signaling; TAS.
DR CO: GO:0009613; P:response to pest/pathogen/parasite; TAS.
DR InterPro: IPR008996; Cytok_IL1 like.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR PRINTS: PR00264; INTERLEUKIN1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; FALSE_NEG.
KW Cytokine; Multigene family.
SQ SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;

Alignment Scores:
Pred. No.: 3,956-14 Length: 169
Score: 229.50 Matches: 56
Percent Similarity: 53.12% Conservative: 29
Best Local Similarity: 35.00% Mismatches: 62
Query Match: 20.24% Indels: 13
DB: 1 Gaps: 5

US-09-869-566-4 (1-650) x 11F9_HUMAN (1-169)
QY 64 GACGATGACGACAAAGCTTGGCGCGCAATTCAGCTCTTGGAGAGTCCAAAGGTGAAG 123
Db 7 AaPaLaAaPpGlyGlyArgAlaValaTyrcGlnSerMetCysLys----- 21
QY 124 AACTTAACCCGAGAAATTCAGATTCATGACAGATCAAGAAAGTACTGCTCGAC 183

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QY 250 ---TCATCTGAGCTCAGCCTCTGCGGAGAAAGAGTTCCTCTGCGGCTCTCT 306  
 Db 74 CysArgAspThrGluPheGlnAsnValIyLysGlyAsnLeuValPheLeuGlyIleLys 93  
 QY 307 AAGGGGAGCTTTGCTCTACTCTGACAAAGATTAAGGCAAGATCATCTCCCTTCAG 366  
 Db 94 AsnArgAsnLeuPheCysCysValGluMetGluGlyLys-----ProThrLeuGln 111  
 QY 367 CTGAAGAAGAGAGAACTGATGAAGCTGGCTGCCCAAGAGATCAGACGCGGCTTC 426  
 Db 112 LeuLysGluValAspIleMetAsnLeuTyrLysGluArgLys---AlaGlnLysAlaPhe 130  
 QY 427 ATCTTTATAGGCTCAGGTGGCTCTCTGACATCTGAGTGGCGGCTCAACCCGGA 486  
 Db 131 LeuPheTyrIleGlyIleGluGlySerThrSerValPheGlnSerValLeuTyrProGly 150  
 QY 487 TGGTTTCATCTGCACCTCC 504  
 Db 151 TTPheIleAlaThrSer 156

## RESULT 9

ILF5\_MOUSE STANDARD; PRT; 156 AA.

ID ILF5\_MOUSE

Q90YI1; Q90YI2;

AC 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Interleukin-1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1

delta) (Interleukin-1-like protein-1) (Interleukin-1-like protein 1)

(IL-1L1) (Interleukin-1 HX1) (IL-1HX1) (Interleukin-1 homolog 3) (IL-

1H3).

GN Name=ILF5; Synonyms=Fl1d, Il1h3, Il1h1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

LN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=21359532; PubMed=11466363;

RA Debers R., Timms J.C., Homey B., Zurawski S., Sana T.R., Lo S.,

RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,

RA Kastelein R.A.;

RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function

as an antagonist and agonist of NF-kappa B activation through the

RT orphan IL-1 receptor-related protein 2.";

RL J. Immunol. 167:1440-1446(2001).

LN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE=20545212; PubMed=11093146;

RA Barton J.L., Herbert R., Bossiolo D., Higgins L., Nicklin M.J.H.;

RA "A tissue specific IL-1 receptor antagonist homolog from the IL-1

RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";

RL Eur. J. Immunol. 30:3299-3308(2000).

LN (3)

RP SEQUENCE FROM N.A.

RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;

RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.;

RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.T., Doyle M.L.,

RA Young P.R.;

RT "Identification and initial characterization of four novel members of

RT the interleukin-1 family.";

RL J. Biol. Chem. 275:10308-10314(2000).

LN (4)

RP SEQUENCE FROM N.A.

RX STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;

RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,

RA Baldirelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisiel K.W.;

RA Blake J.A., Bradt D., Brusie V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Girimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempole C.A., Seou M., Shimada K.,  
 RA Sulrana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilting L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

CC -I- FUNCTION: Is a highly and a specific antagonist of the IL-1

CC receptor-related protein 2-mediated response to Interleukin 1

CC family member 9 (IL1F9). Could constitute part of an independent

CC signaling system analogous to interleukin-1 alpha (IL-1A), beta

CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-

CC 1R1), that is present in epithelial barriers and takes part in

CC local inflammatory response (by similarity).

CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -I- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and

CC tissues containing epithelial cells.

CC -I- SIMILARITY: Belongs to the IL-1 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL; AF230378; AAF91275.1; -

DR EMBL; AK009741; BAB26471.1; -

DR EMBL; AK008977; BAB26002.1; -

DR EMBL; AJ250429; CAB59831.1; ALT\_INIT.

DR EMBL; AF200495; AAF69251.1; -

DR PDB; 1MD6; X-ray; A=3-156.

DR MGD; MGI:1859325; Il1f5.

DR InterPro; IPR008996; CytoK IL1 like.

DR InterPro; IPR000975; Interleukin\_1.

DR Pfam; PR00340; IL1; 1

DR PRINTS; PR00264; INTERLEUKIN1.

DR ProDom; PDO02536; Interleukin\_1; 1.

DR SMART; SM00125; IL1; 1.

DR PROSITE; PS00253; INTERLEUKIN\_1; 1.

KW 3D-structure; Cytokine; Multigene family.

FT CONFLICT 2 Missing (in Ref. 3).

FT SEQUENCE 156 AA; 17136 MW; A4D1E2F93CF77A7 CRC64;

Alignment Scores:

Pred. No.: 2,666-10 Length: 156

Score: 191.50 Matches: 53

Percent Similarity: 50.99% Conservative: 24

Best Local Similarity: 35.10% Mismatches: 51

Query Match: 16.89% Indels: 23

DB: 1 Gaps: 6

US-09-869-566-4 (1-650) x ILF5\_MOUSE (1-156)

QY 91 AATTCAGCTCTTGGACGAGCTCCAAAGGTGAAGAACTTAAACCGAAGAAATTTCAGATT 150



```

Db      5 SerGlyAlaLeuCyS-----PheArgMet 12
QY      151 CATGACACAGATCACAAGTATGCTGCTGACTCTGGAAATCTCATAGA-----GTT 204
Db      13 LysAspSerAlaLeuLysValLeuLysHISAsnAsnGlnLeuLeuLysGlyLeu 32
QY      205 CCAGATTAACATACATACAGCCAGATCTTCTTGATAGCTCATCTGAGCTCA 264
Db      33 HIsAlaGlnLysValLysGlyLysGlnLysLeuValProAsnArgHIsAlaLeuAsp 52
QY      265 GCCTCTGCCGAGAAAGAAAGTCCGATTCTCTGGGGCTCTTAAAGGGAAGTTTGCTTC 324
Db      53 AlaSerLeu-----SerProValIleLeuGlyValGlnGlyLysGlnCysLeu 69
QY      325 TACTGTGACAGAGTAAGACAAAGTATCATCTCCCTTCACTGAGTAAAGAGAAACATG 384
Db      70 SerCyGlyThrGlnLysGly-----ProIleLeuLysLeuLysProValAsnIle 86
QY      385 ATGAAGCTG---GCTGCCAAAGAAAGATGACGACGCCGCCCTTCATCTTTATAGGGCT 441
Db      87 MetGlnLeuThrLysGlnGlyAlaLysGlnSer-----LysSerPheThrPheThrArg 104
QY      442 CAGGTGGGCTCTCGAATGCTGAGTGGCGGCTCACCCCGAGTGTTCATCTGACACC 501
Db      105 AspMetGlyLeuThrSerSerPheGlnSerAlaAlaIleThrProGlyThrPheLeuGlyThr 124
QY      502 TCCCTGCATTTGATGAGCTGTGGGGTGACA 534
Db      125 SerProGlnAlaAspGlnProValArgLeuThr 135

RESULT 10
Q6UVX7 PRELIMINARY; PRT; 134 AA.
AC 06UVX7;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE IRA2.
DE ORFNames=UNQ2456;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Batton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehnagiri S., Simmons L., Singh J., Smith V., Stinson J., Vastis A.,
RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
CC -1 SIMILARITY: Belongs to the IL-1 family.
DR EMBL: AY59111; AAC09469.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005152; F:interleukin-1 receptor antagonist activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR008996; Cyclo IL1 like.
DR InterPro: IPR003297; InterleukinIL1RA.
DR InterPro: IPR000975; Interleukin_1.
DR PRINTS: PRO0264; INTERLEUKIN1.
DR PRINTS: PRO1360; INTERLEUKINX.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
SQ SEQUENCE 134 AA; 14928 MW; D5369C5AD44A9752 CRC64;

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Alignment Scores:
Pred. No.: 3,68e-10 Length: 134
Score: 190.00 Matches: 40
Percent Similarity: 64.778 Conservative: 17
Best Local Similarity: 45.458 Mismatches: 27
Query Match: 16.754 Indels: 4
DB: 2 Gaps: 3

US-09-869-566-4 (1-650) x Q6UVX7 (1-134)
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Db 36 ArgGlyAspProIleThrLeuGlyIleGlnAsnProGluMetCysLeuThrCysGlyLys 55
QY 337 GATTAAGACAAAGTATCATCTCCCTTCACTGAGTAAAGAGAAACTGATGAAGCTGCT 396
Db 56 ValGlyGlnGln-----ProThrLeuGlnLeuLysGlnGlnLysIleMetAspLeuThr 73
QY 397 GCCAAAGAAAGTACAGACAGCCGCCCTTCATCTTTATAGGGGCTCAGGTGGGCTCTGG 456
Db 74 GlyGlnProGlnProVal---LysProPheLeuPheThrArgAlaLysThrGlyArgThr 92
QY 457 AACATGCTGAGTCCGCGGCTCACCCCGAGTGTTCATCTGACACTCTGCAATTGTAAT 516
Db 93 SerThrLeuGlnSerValAlaLysPheProAspThrPheIleAlaSerSer---LysArgAsp 111
QY 517 GAGCCTGTTGGGGTGACAGATAA 540
Db 112 GlnProIleIleLeuThrSerGln 119

RESULT 11
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AC Q9UBH0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin 1 family member 5 (IL-1F5) (interleukin-1 delta (IL-1
DE delta) (Fli1 delta) (interleukin-1-like protein 1) (IL-1L1)
DE (interleukin-1 HVI) (IL-1HVI) (interleukin-1 receptor antagonist
DE homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3)
DE (UNQ1896/PRO4342).
GN Name=I1F5; Synonyms=FIL1D, IL1HVI, IL1L1, IL1RP3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
RA Sims J.E.;
RT "Four new members expand the IL-1 superfamily."
RT J. Biol. Chem. 275:1169-1175(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal skin;
RX MEDLINE=9943727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
RA Dymnac R., Ford J.E.;
RT "IL1HVI, a novel interleukin-1 receptor antagonist gene."
RT Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20545212; PubMed=11093146;
RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
RA Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J.H.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities."
RL Eur. J. Immunol. 30:3299-3308(2000).

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RP [4] SEQUENCE FROM N.A.  
RX MEDLINE=21359532; PubMed=11446363;  
RA Dbeets R., Timans J.C., Homay B., Zurawski S., Sana T.R., Lo S.,  
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,  
RA Kastelein R.A.;  
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function  
RT as an antagonist and agonist of NF-kappa B activation through the  
RT orphan IL-1 receptor-related protein 2.";  
RL J. Immunol. 167:1440-1446(2001).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;  
RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,  
RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;  
RT "Identification and gene organization of three novel members of the  
RT IL-1 family on human chromosome 2.";  
RL Genomics 66:213-216(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Sehagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagstad A.,  
RA Vanden R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.L., Fengold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshimiyuki S., Barnhill P., Prange C.,  
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywnski M.I., Skalska U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Is a highly and a specific antagonist of the IL-1  
CC receptor-related protein 2-mediated response to interleukin 1  
CC family member 9 (IL1F9). Could constitute part of an independent  
CC signaling system analogous to interleukin-1 alpha (IL-1A), beta  
CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-  
CC 1R1), that is present in epithelial barriers and takes part in  
CC local inflammatory response.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but  
CC not in fibroblasts, endothelial cells or melanocytes. Detected  
CC also in the spleen, brain leukocyte and macrophage cell types.  
CC Increased in lesional psoriasis skin.  
CC -1- INDUCTION: By phorbol ester (PMA) and lipopolysaccharide (LPS)  
CC treatment in macrophage cell line.  
CC -1- SIMILARITY: Belongs to the IL-1 family.

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CC -----
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CC -----
DR EMBL, AF01830, AAF25210.1, -
DR EMBL, AF16094, AAF2757.1, -
DR EMBL, AJ242737, CAB59822.1, -
DR EMBL, AJ242738, CAB59823.1, -
DR EMBL, AJ271338, CAB67704.1, -
DR EMBL, AF216693, AAF76981.1, -
DR EMBL, AF230377, AAF91274.1, -
DR EMBL, AY359117, AAO89475.1, -
DR EMBL, BC024747, AAH24747.1, -
DR PIR, JC7104, JC7104, -
DR HSSP, P18510, 11LR, -
DR Genew, HGNC:15561, IL1F5, -
DR MIM, 605507, -, -
DR GO, GO:0005152, P.interleukin-1 receptor antagonist activity, TAS, -
DR InterPro, IPR008986, CytoK_IL1_like, -
DR InterPro, IPR000975, Interleukin_1, -
DR Pfam, PF00340, IL1, 1, -
DR PRINTS, PR00264, INTERLEUKIN1, -
DR Prodom, PD002536, interleukin_1, 1, -
DR SMART, SM00125, IL1, 1, -
DR PROSITE, PS00253, INTERLEUKIN_1, 1, -
DR Cytokine, Multigene family, -
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Alignment Scores:
Pred. No.: 1,38e-08 Length: 155
Score: 174.50 Matches: 54
Best Local Similarity: 42.60% Conservative: 18
Best Local Similarity: 31.95% Mismatches: 48
Query Match: 15.39% Indels: 49
DB: 1 Gaps: 7
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DB 4 SerGlyAlaLeuCys-----PheArgMet 11
QY 151 CATGACCAAGATTCACAAAGTACTGTGGTCTCTGACATCTGGGAATTCATGACAGTTCCAGAT 210
DB 12 LysAspSerAlaLeuLysValLeuTyrLeuHisAsnAsnGlnLeu----- 26
QY 211 AAAAACTACATACGCCCCAGACAGATCTTTGGCATTAAGCTTACTCTTGAGCTCAGACCTT 270
DB 27 -----LeuAlaGlyLeuHisAlaGlyLys 35
QY 271 GCGGAGAAAGA-----AGT 285
DB 36 ValLeuLysGlyGlnGlnIleSerValProAsnArgTyrLeuAspAlaSerLeuSer 55
QY 286 CGGATTCCTCGGGGGGCTCTTAAAGGGGAGTTTGTCTCTACTGTGACAAAGATTAAGGA 345
DB 56 ProValIleLeuGlyValGlnGlyLysArgGlnCysLeuSerCys-----GlyValGly 73
QY 346 CAAGATCATCAATCCCTTCAGCTGGAAGAGAAAGAACTGATGAAGCTG--GCTGCCAA 402
DB 74 Gln---GluProThrLeuThrLeuGluProValAsnIleMetGluLeuTyrLeuGlyAla 92
QY 403 AAGGAATGAGACAGCCGCGCCTTATCTTTTATAGAGGCTCAGGTGGGCTCTCGAACAATG 462
DB 93 LysGlnSer-----LysSerPheThrPheTyrArgAspArgMetGlyLeuThrSerSer 110
QY 463 CTGAGAGTGGGGGGCTACCCCGGAGATGATTCATGTGACATCTCTGCAATTGTAATAGGCT 522

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DB 111 pNegIuserAlaIatYrProgiYrTpPhLeuCyThrValProGIuAlaSepGIInPro 130  
 QY 523 GTTGGGTCAGACATTAATTGGAGAC 549  
 DB 131 ValArgLeuThrGIuLeuProGIuAen 139  
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 AC Q7RTZ6;  
 DT 01-MAR-2004 (TEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE IL-1P5 (IL-1HY, FIIL-delta, IL-1RP3, IL-1IL1, IL-1-delta).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20545212; PubMed=11093146;  
 RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMUJ3299>3.0.CO;2-S;  
 RA Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J.;  
 RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1  
 RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities";  
 RL Eur. J. Immunol. 30:3299-3308(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97312693; PubMed=91619134; DOI=10.1006/geno.1997.4654;  
 RA Notwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,  
 RA Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,  
 RA Hildebrandt F.;  
 RT "Molecular cloning of the interleukin-1 gene cluster: construction of  
 RT an integrated YAC/PAC contig and a partial transcriptional map in the  
 RT region of chromosome 2q13.";  
 RL Genomics 41:370-378(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94245215; PubMed=8188271;  
 RA Nicklin M.J.H., Welch A., Duff G.W.;  
 RT "A physical map of the region encompassing the human interleukin-1-  
 RT alpha, interleukin-1-beta and interleukin-1 receptor genes";  
 RL Genomics 19:382-384(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;  
 RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,  
 RA Korman K.;  
 RT "A sequence-based map of the nine genes of the human interleukin-1  
 RT cluster";  
 RL Genomics 79:718-725(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/dbrc.1999.1440;  
 RA Mulero J.J., Pace A.M., Nelson S.T., Loeb D.D., Correa T.R.,  
 RA Dmanac R., Ford J.E.;  
 RT "IL1HY: A novel interleukin-1 receptor antagonist gene";  
 RL Biochem. Biophys. Res. Commun. 263:702-706(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;  
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kudin M., Garika K.E.,  
 RA Sims J.E.;  
 RT "Four new members expand the interleukin-1 superfamily.";  
 RL J. Biol. Chem. 275:1169-1175(2000).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;  
 RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
 RA Griswold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L.,  
 RA Young P.R.;  
 RT "Identification and initial characterization of four novel members of  
 RT the interleukin-1 family.";

RL J. Biol. Chem. 275:10308-10314(2000).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;  
 RA Busfield S.J., Comrack C.A., Yu G., Chikering T.W., Smutko J.S.,  
 RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;  
 RT "Identification and gene organization of three novel members of the  
 RT IL-1 family on human chromosome 2.";  
 RL Genomics 66:213-216(2000).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21065522; PubMed=11145836; DOI=10.1006/cyto.2000.0799;  
 RA Pan G., Risser P., Mo W., Baldwin D.T., Zhong A.W., Flivoroff B.,  
 RA Yansura D., Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R.;  
 RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-  
 RT 1Rtp.";  
 RL Cytokine 13:1-7(2001).  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;  
 RA Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J.,  
 RA Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;  
 RT "Cloning and characterization of IL-1HY2, a novel interleukin-1 family  
 RT member.";  
 RL J. Biol. Chem. 276:20597-20602(2001).  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21359532; PubMed=11466363;  
 RA Debetts R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,  
 RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,  
 RA Kastelein R.A.;  
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function  
 RT as an antagonist and agonist of NF-kB activation through the orphan  
 RT IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.";  
 RL J. Immunol. 167:1440-1446(2001).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3;  
 RA Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,  
 RA Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G.,  
 RA Pan Y., Smith D.E., Young P.R.;  
 RT "A new nomenclature for the IL-1-family genes";  
 RL Trends Immunol. 22:536-537(2001).  
 CC -I- MISCELLANEOUS: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBD third party annotation (TPA) entry.  
 CC -I- SIMILARITY: Belongs to the IL-1 family.  
 DR EMBL; BN000002; CAD29877.1; -.  
 DR HSP; OQ0Y1; IM06.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005152; P:interleukin-1 receptor antagonist activity; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0006954; P:inflammatory response; IEA.  
 DR InterPro; IPR008996; Cytok IL1 like.  
 DR InterPro; IPR003296; InterleukinIL1B.  
 DR InterPro; IPR003297; InterleukinIL1RA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR PRINTS; PR00264; INTERLEUKIN1.  
 DR PRINTS; PR01359; INTERLEUKIN1B.  
 DR PRINTS; PR01360; INTERLEUKIN1X.  
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 DR PROSITE; PS00253; INTERLEUKIN\_1; UNKNOWN 1.  
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## Alignment Scores:

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Score:	174.50	Matches:	54
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Query Match:	15.39%	Indels:	49
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US-09-869-566-4 (1-650) x Q7RTZ6 (1-155)



RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toehlyki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mulaly S.J.,  
 RA Bosak S.A., McMan K.C., McKernan K.J., Malek J.A., Gamarale P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skaleka U., Smalins D.E., Schmeich A., Schein J.E.,  
 RA Jones S.J., Maitra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;  
 RA Strausberg R.;  
 CC Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the IL-1 family.  
 DR EMBL: BC042532; AAH42532.1; -  
 DR HSSP: P18510; 11LR.  
 DR MGD: MGI:96547; 11LR.  
 DR GO: GO:0030073; P:insulin secretion; IMP.  
 DR GO: GO:0006629; P:lipid metabolism; IMP.  
 DR InterPro: IPR008996; CytoC IL1 like.  
 DR InterPro: IPR003297; Interleukin1LRA.  
 DR InterPro: IPR000975; Interleukin\_1.  
 DR Pfam: PF00340; IL1; 1.  
 DR PRINTS: PR00264; INTERLEUKIN1.  
 DR PRINTS: PR01360; INTERLEUKINX.  
 DR ProDom: PD002536; Interleukin\_1, 1.  
 DR SMART: SM00125; IL1; 1.  
 DR PROSITE: PS00253; INTERLEUKIN\_1; 1.  
 KM Receptor.  
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 QY 445 GTGGGCTCTCTGGAACATGCTGAGTGGCGGCTACCCCGAGATGTTTCATCTGCACCTCC 504  
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 QY 505 TCGAATTTGTAATGACCTGTTGGGCTGACAGATTAATTTGAGAACAGAAACATT--- 561  
 DB 132 LeuGlnAlaAspArgProValSerIleThrAsnThrProGlnGlnProleuIleValThr 151  
 QY 562 GAATTTTCATTTCA 576  
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 RESULT 15  
 ID 11F6 MOUSE STANDARD; PRT; 160 AA.  
 AC 09JLA2;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin 1 family member 6 (IL-1F6) (Interleukin-1 epsilon) (IL-1 epsilon) (Frl1 epsilon) (Interleukin-1 homolog 1) (IL-1H1).  
 OS Name=11f6; Synonyms=F11e, I11e, I11h1;  
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 RN [1]  
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 RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;  
 RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
 RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,  
 RA Young P.R.;  
 RT "Identification and initial characterization of four novel members of  
 RT the interleukin-1 family";  
 RL J. Biol. Chem. 275:10308-10314(2000).  
 RN [2]  
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 RX MEDLINE=21359532; PubMed=11466363;  
 RA Debers R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,  
 RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,  
 RA Kastelein R.A.;  
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function  
 RT as an antagonist and agonist of NF-kappa B activation through the  
 RT orphan IL-1 receptor-related protein 2";  
 RL J. Immunol. 167:1440-1446(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Oasato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Nagai K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,  
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser J.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedziarski R.M., King B.L.,  
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.D., Pereira G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravesi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watnabe Y., Wells C.,  
 RA Wilming L.G., Wyszaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs";  
RL Nature 420:563-573 (2002).  
CC - TISSUE SPECIFICITY: Secreted (Potential).  
CC - TISSUE SPECIFICITY: Highly expressed in embryonic tissue and in  
CC tissues containing epithelial cells.  
CC - MISCELLANEOUS: Binding analysis failed to detect interaction with  
CC multiple IL1R family members.  
CC - SIMILARITY: Belongs to the IL-1 family.  
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR MGD; MGI:1859324; I11f6.  
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OY 175 GTCCCTGGACTCTGGGATCTCATGACAGTTCAGATAAATACTACGCCAGAGATC 234  
DB 26 I1eLeuGlnaIaSerLeuThrIaIaValProArgIaIaSerGlnIaIaThrValProValThr 45  
OY 235 TTCTTTGCAATTA--GCCATCATCTTGAAGCTCAGCTCGCGGAGAAAGGAAGTCCGATT 291  
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OY 352 CATTCATCCCTTGAAGTGAAGAAAGAACTGATGAAGCTGGCTGCCAAAGGAATCA 411  
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DB 104 ValIaIaSer---LeuPheYrHISlyIaIaSerGlyThrThrSerThrPheGlnSer 122

OY 472 GCGGCTACCCCGGATGGTTCATC-----TGCACCTCTCTGCATTTGT 513  
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Search completed: May 28, 2005, 17:38:39  
Job time : 98.5 secs

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4	517	79.5	847	6	AX133934	AX133934 Sequence
5	517	79.5	847	6	BD014862	BD014862 Polypepti
6	517	79.5	855	6	AX133936	AX133936 Sequence
7	517	79.5	855	6	BD014863	BD014863 Polypepti
8	517	79.5	1104	6	BD017454	BD017454 Protein b
9	516.8	79.5	787	6	AF167368	AF167368 Homo sapi
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41	367.8	56.6	654	6	BD242670	BD251975	IL-1 zeta
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39	392.2	60.3	501	6	BD080411	BD251975	IL-1 zeta
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36	394	60.6	474	6	BD251976	AY071840	Homo sapi
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34	396.6	61.0	636	6	BD242668	AY071840	Homo sapi
33	396.6	61.0	537	9	AF251120	AY071840	Homo sapi
32	397	76.1	989	6	BD080409	AY071840	Homo sapi
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24	513.6	79.0	630	6	BD276577	AY071840	Homo sapi
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ACCESSION	BD263568			
VERSION	BD263568.1	GI:33073336		
KEYWORDS	JP 200253122-A/2.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	other sequences; artificial sequences.			
AUTHORS	1. (bases 1 to 650)			
TITLE	Goddard, A. and Pan, J.			
JOURNAL	IL-1 related polypeptides			
	Patent: JP 200253122-A 2 08-OCT-2002;			

**COMMENT**

PN JP 200253122-A/2  
PD 08-OCT-2002  
PR 22-DEC-1998 JP 2000591188  
PR 23-DEC-1998 US 60/113430, 22-JAN-1999 US 60/116843 PR  
13-APR-1999 US 60/129122  
PI ADRES GODDARD, JAMES PAN  
C1 C12N1/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC

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VERSION JP 2002533122-A/1.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1006)  
AUTHORS Goddard, A. and Pan, J.  
TITLE IL-1 related polypeptides  
JOURNAL Patient: JP 2002533122-A 1 08-OCT-2002;  
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PC C12N5/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
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CC IL-1 related polypeptides  
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FT /organism='Homo sapiens (human)'.

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Location/Qualifiers  
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Oy 154 GACGAGATCACAAAGTACTGCTCTGAGCTCTGGAATCTCATAGCAGTTCCAGATTA 213  
Db 469 GACGAGATCACAAAGTACTGCTCTGAGCTCTGGAATCTCATAGCAGTTCCAGATTA 528  
Oy 214 AACTACATAGCCCGCAGAGATCTTCTTTGCAATTAAGCTCATCTTGAAGTCAAGCTCTGCG 273  
Db 529 AACTACATAGCCCGCAGAGATCTTCTTTGCAATTAAGCTCATCTTGAAGTCAAGCTCTGCG 588  
Oy 274 GAGAAAGGAAGTCCGATTTCTCTGGGGGTCTTAAAGGGAGTTTGTCTCTACTGTAC 333  
Db 589 GAGAAAGGAAGTCCGATTTCTCTGGGGGTCTTAAAGGGAGTTTGTCTCTACTGTAC 648  
Oy 334 AAGATTAAGGACAAAGTCAATCCATCCCTGAGCTGAAGAGAGAACTGATGAAGCTG 393  
Db 649 AAGATTAAGGACAAAGTCAATCCATCCCTGAGCTGAAGAGAGAACTGATGAAGCTG 708  
Oy 394 GCTGCCCAAAAGGAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCC 453  
Db 709 GCTGCCCAAAAGGAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCC 768  
Oy 454 TGGAAATGCTGGAAGTCCGCGGCTCAACCCCGGATGCTTCACTGACCTCTCGCAATGT 513  
Db 769 TGGAAATGCTGGAAGTCCGCGGCTCAACCCCGGATGCTTCACTGACCTCTCGCAATGT 828  
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VERSION MGC.  
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SOURCE MGC.  
ORGANISM Homo sapiens (human)  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 760)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, J., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Umedu, T.B., Toshilyak, S., Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gumaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,



FAHEY, J., HELTON, E., KETTEMAN, M., MADAN, A., RODRIGUES, S.,  
SANCHEZ, A., WHITING, M., MADAN, A., YOUNG, A.C., SHEVCHENKO, Y.,  
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BUTTERFIELD, Y.S., KRZYWINSKI, M.I., SKALSKA, U., SMALL, D.E.,  
SCHNECH, A., SCHEIN, J.E., JONES, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 760)  
Strasbourg, R.  
Direct Submission  
Submitted (03-JAN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: CLONTECH  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAL Plate: 37 Row: h Column: 22  
This clone was selected for full length sequencing because it  
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ACCESSION AX133934  
VERSION AX133934.1 GI:14139876  
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ORGANISM Homo sapiens (human)  
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Ushio, S., Nukada, Y., Yamamoto, K. and Kurimoto, M.  
TITLE Polypeptide and uses thereof  
JOURNAL Patent: EP 1092773-A 4 18-APR-2001;  
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)  
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 KEYWORDS JP 2001178479-A/5.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 1 (bases 1 to 855)  
 Uehio, S., Nukata, Y., Yamamoto, K. and Kurimono, M.  
 Polypeptide and utilization thereof  
 Patent: JP 2001178479-A 5 03-JUL-2001;  
 HAYASHIBARA BIOCHEMICAL LABORATORIES INC DIRECTOR GENERAL OF  
 NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND  
 OS Homo sapiens (human)  
 PN JP 2001178479-A/5  
 PD 03-JUL-2001  
 PF 13-OCT-2000 JP 2000312761  
 PI SHINBEI USHIO,YOSHITUKI NUKATA,KOZO YAMAMOTO,MASASHI KURIMOTO  
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 PC C07K14/545,  
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 1 (bases 1 to 1104)  
 Matsushita, T., Sakakibara, T., Sekine, S., Sato, M., Sakurai, S. and  
 Furuya, A.  
 Protein belonging to IL-1family  
 Patent: JP 2001231578-A 2 28-AUG-2001;  
 KYOMA HAKKO KOGYO CO LTD

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	PI	TAKESHI MATSUSHITA, TOSHIRO SAKAKIBARA, SUSUMU SEKINE, MITSUO
	PI	SAITO,
	PI	SATORU SAKURAI, AKIKO FURUYA
	PC	C12N5/09 A01K67/027, A61K31/711, A61K38/00, A61K39/335, A61K48/00,
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ACCESSION AF200496.1 GI:7769119  
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1 (bases 1 to 793)  
Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,  
Griswold,D.E., Capper,E.A., Tai-Singer,R., Wells,G.I., Doyle,M.L.  
and Young,P.R.  
TITLE Identification and initial characterization of four novel members  
of the interleukin-1 family  
JOURNAL J. Biol. Chem. 275 (14), 10308-10314 (2000)  
MEDLINE 20209405  
PUBMED 10744718  
REFERENCE 2 (bases 1 to 793)  
AUTHORS Kumar,S., McDonnell,P.C. and Young,P.R.  
TITLE Direct Submission  
JOURNAL Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,  
SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of  
Prussia, PA 19406, USA  
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Qy 339 TAAAGCACAAGTCAATCCATCCCTTCAGCTGAAGAGAAATGATGAAGCTGGCTC 398  
Db 423 TAAAGCACAAGTCAATCCATCCCTTCAGCTGAAGAGAAATGATGAAGCTGGCTC 482

Qy 399 CCAAAAGGATGACACGCGCGCCCTTCATCTTTATAGGGCTCAGTGGGCTCTGGAA 458  
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Db 603 GCTGTGGGGTGAAGATTAATTTGAGAACAGAAACATTTGATTTCAATTTCAAC 662

Qy 579 AGTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAGAGTAC 626  
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RESULT 11  
AR183757 802 bp DNA linear PAT 20-APR-2002  
LOCUS AR183757  
DEFINITION Sequence 1 from patent US 6342371.  
ACCESSION AR183757  
VERSION AR183757.1 GI:20227726  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 802)  
AUTHORS McDonnell,P.C. and Young,P.R.  
TITLE Interleukin-1 homologue, IL-1H4  
JOURNAL Patent: US 6342371-A 1 29-JAN-2002;  
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Query Match 79.5%; Score 516.8; DB 6; Length 802;  
Best Local Similarity 98.7%; Pred. No.1.6e-141;  
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 99 TCTTTCAGAGGTCCTCAAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTATGACCA 158  
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Qy 159 GGATCACAAGATGATCGTCTGGAGTCTGGGAATTCATAGCATTCCAGATTAATACTA 218  
Db 252 GGATCACAAGATGATCGTCTGGAGTCTGGGAATTCATAGCATTCCAGATTAATACTA 311

Qy 219 CATAGCCCAAGATCTTCTTGGCATTTAGCCTCATCTTGAAGTCAAGCTTCGCGAGAA 278  
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Qy 279 AGAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTGACAGAA 338  
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QY 519 GCGTGTGGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAATTCACC 578
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QY 579 AGTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCTTATGAGGTAC 626
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RESULT 12
AF251118 817 bp mRNA linear PRI 03-MAY-2001
LOCUS AF251118
DEFINITION Homo sapiens interleukin-1-related protein long isoform a mRNA,
complete cds; alternatively spliced.
ACCESSION AF251118
VERSION AF251118.1 GI:10185735
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 817)
Pan, G., Risser, P., Mao, W., Baldwin, D.T., Zhong, A.W., Filvaroff, E.,
Yansura, D., Lewis, L., Eigenbrodt, C., Henzel, W.J., and Vanden, R.
IL-1H, an interleukin-1-related protein that binds IL-18
receptor/IL-1Rrp
CYTOKINE 13 (1), 1-7 (2001)
JOURNAL 1145836
MEDLINE 2106552
PUBMED 11145836
REFERENCE 2 (bases 1 to 817)
Pan, G., Baldwin, D.T., and Zhong, A.W.
Direct Submission
Submitted (03-APR-2000) Endocrinology, Genentech, Inc., 1 DNA Way,
South San Francisco, CA 94080, USA
JOURNAL location/Qualifiers
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ORIGIN
Query Match 79.5%; Score 516.8; DB 9; Length 817;
Best Local Similarity 98.7%; Pred. No. 1.6e-141;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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DB 627 GCGTGTGGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAATTCACC 686
QY 579 AGTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCTTATGAGGTAC 626
DB 687 AGTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCTTATGAGGTAC 734

RESULT 13
BD263581 839 bp DNA linear PAT 17-JUL-2003
LOCUS BD263581
DEFINITION IL-1 related polypeptides.
ACCESSION BD263581
VERSION BD263581.1 GI:33073349
KEYWORDS JP 2002533122-A/15.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 839)
Goddard, A. and Pan, J.
IL-1 related polypeptides
Patent: JP 2002533122-A 15 08-OCT-2002;
JOURNAL GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002533122-A/15
PD 08-OCT-2002
PF 22-DEC-1999 JP 2000591188
PR 23-DEC-1998 US 60/113430.22-JAN-1999 US 60/116843 PR
PI 13-APR-1999 US 60/129122
PI ANDREY GODDARD, JAMES PAN
PC C12N15/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10.
PC C12P21/02, C12P21/08, C12N15/00, C12N5/00
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FH Key Location/Qualifiers
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Best Local Similarity 98.7%; Pred. No. 1.6e-141;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Db 627 GCCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGAAATTTTCAATTTCAAC 686  
Qy 579 AGTTTGCAAAGCTGAATGAGCCCGAGTGAGGTCAAGCGATTAGGGTAC 626  
Db 687 AGTTTGCAAAGCTGAATGAGCCCGAGTGAGGTCAAGCGATTAGGAAC 734

RESULT 14  
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LOCUS Interleukin-1 homolog ZIL1A4.  
DEFINITION BD242667.1 GI:33052437  
ACCESSION BD242667.1 GI:33052437  
VERSION JP 2002528079-A/1.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 1600)  
REFERENCE Weet,R.R., Sheppard,P.O. and Gao,Z.  
AUTHORS Interleukin-1 homolog ZIL1A4  
TITLE Patent: JP 2002528079-A 1 03-SEP-2002;  
JOURNAL ZYMOGENETICS INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002528079-A/1  
PD 03-SEP-2002  
PF 27-OCT-1999 JP 2000578451  
PR 27-OCT-1998 US 09/179614  
PI ROBERT R WEET, PAUL O SHEPPARD, ZEREN GAO  
PC C12N15/09,A61K38/00,A61P37/02,C07K14/545,C12N1/15,C12N1/19, PC  
C12N1/21,  
PC C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC  
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Query Match 79.5%; Score 516.8; DB 6; Length 1600;  
Best Local Similarity 98.7%; Pred. No. 1.7e-141;  
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Qy 279 AGAAGTCCGATTCCTGCGGGGCTCTTAAGGGAGTTTGTCTCTACTGACGAAGA 338  
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Qy 339 TAAAGACAAAGTTCATCCCTTCAGCTGAGAAAGAAACTGATGAAGCTGCTGC 398  
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Db 1401 GCCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGAAATTTTCAATTTCAAC 1460  
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RESULT 15  
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ACCESSION BD251972.1 GI:33061742  
VERSION JP 2002532094-A/1.  
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SOURCE Homo sapiens  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 579)  
REFERENCE Sims,J.E., Smith,D.E. and Born,T.L.  
AUTHORS IL-1 zeta, IL-1 zeta splice variants and Xrec2 DNAs and  
TITLE polypeptides  
JOURNAL Patent: JP 2002532094-A 1 02-OCT-2002;  
COMMENT OS Homo sapiens (human)  
PN JP 2002532094-A/1  
PD 02-OCT-2002  
PF 14-DEC-1999 JP 2000588357  
PR 14-DEC-1998 US 60/112163, 10-NOV-1999 US 60/164675 PI  
JOHN E SIMS, DIRK E SMITH, TERESA L BORN  
PC C12N15/09,C07K14/47,C07K14/715,C07K16/24,C07K16/28,C12N1/15,  
PC C12N1/19,C12N5/10,C12P21/02,C12P21/08,C12N15/00,C12N5/00 CC  
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XX  P-PSDB; AAY96933.
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XX  Nucleic acids encoding interleukin-1-like polypeptides, useful for
XX  preventing and treating e.g. inflammation, asthma and psoriasis.
XX
XX  Claim 7; Fig 2; 143pp; English.
XX
XX  An isolated nucleic acid molecule encoding an interleukin-1-like
XX  polypeptide (IL-11p) that retains one or more activities of the peptide
XX  from which it is derived, such as the IL-18R binding activity of a human
XX  interleukin-1 receptor antagonist-1 (IL-1Ra1) polypeptide, is new. The
XX  nucleic acids may be used in molecular engineering applications, e.g.
XX  hybridization assays and chromosome and gene mapping studies, for
XX  recombinantly producing the IL-11p polypeptide or for producing gene
XX  knock out animals to study the role of the protein in metabolism and
XX  disease processes (conversely, gene therapy protocols may be used to
XX  supplement a patient's production of the polypeptide or to rectify
XX  mutations that lead to the production of an active peptide). The
XX  peptides produced may be used to screen for and produce modulators (e.g.
XX  antibodies) of IL-11p protein expression and activity which may be used to
XX  treat disorders associated with inappropriate IL-11p expression and
XX  activity, such as inflammatory disorders, asthma, arthritis,
XX  osteoarthritis, sepsis, acute lung injury, adult respiratory distress
XX  syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
XX  psoriasis, graft versus host disease and/or inflammatory bowel disease
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XX  dermatological; immunomodulatory; gastrointestinal; gene therapy; ds.
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XX  PR  13-APR-1999; 99US-0129122P.
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XX  (GETH ) GENENTECH INC.
XX
XX  Goddard A, Pan J;
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XX  MPI: 2000-452395/39.
XX  P-PSDB; AAY96931, AAY96932.
XX
XX  Nucleic acids encoding interleukin-1-like polypeptides, useful for
XX  preventing and treating e.g. inflammation, asthma and psoriasis.
XX
XX  Example 1; Fig 1A-B; 143pp; English.
XX
XX  An isolated nucleic acid molecule encoding an interleukin-1-like
XX  polypeptide (IL-11p) that retains one or more activities of the peptide
XX  from which it is derived, such as the IL-18R binding activity of a human
XX  interleukin-1 receptor antagonist-1 (IL-1Ra1) polypeptide, is new. The
XX  nucleic acids may be used in molecular engineering applications, e.g.
XX  hybridization assays and chromosome and gene mapping studies, for
XX  recombinantly producing the IL-11p polypeptide or for producing gene
XX  knock out animals to study the role of the protein in metabolism and
XX  disease processes (conversely, gene therapy protocols may be used to
XX  supplement a patient's production of the polypeptide or to rectify
XX  mutations that lead to the production of an active peptide). The
XX  peptides produced may be used to screen for and produce modulators (e.g.
XX  antibodies) of IL-11p protein expression and activity which may be used to
XX  treat disorders associated with inappropriate IL-11p expression and
XX  activity, such as inflammatory disorders, asthma, arthritis,
XX  osteoarthritis, sepsis, acute lung injury, adult respiratory distress
XX

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useful  
killer

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XX AC AAI71179;
XX DT 22-JAN-2002 (first entry)
XX DE Human interleukin 1 family protein encoding cDNA SEQ ID NO:4.
XX DE Human interleukin 1; IL-1; growth factor; Tango-77; diagnosis;
XX KW Human; interleukin 1; IL-1; growth factor; Tango-77; diagnosis;
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XX OS Homo sapiens.
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XX FT /tag= a
XX FT /product= "IL-1 family protein"
XX PN JP2001231578-A.
XX PD 28-AUG-2001.
XX PF 07-DEC-2000; 2000JP-00372864.
XX PR 09-DEC-1999; 99JP-00349780.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX DR WPI, 2001-609968/70.
XX DR P-PSDB; AAG68116.
XX PT An IL-1 family protein, used for the development of diagnostic and
XX PT treatment agents.
XX PS Claim 2; Page 31-32; 38pp; Japanese.
XX CC The present sequence encodes a human interleukin 1 (IL-1) family protein
XX CC having a combining affinity to a receptor of a protein of human IL-1
XX CC family higher than Tango-77. The protein is useful for the development of
XX CC diagnostic, treating and/or preventive agents for various diseases
XX SQ Sequence 1104 BP; 328 A; 258 C; 255 G; 263 T; 0 U; 0 Other;

Query Match 79.5%; Score 517; DB 4; Length 1104;
Best Local Similarity 97.2%; Pred. No. 4,6e-159;
Matches 526; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 86 CCGCGAATTCAGCTCTTTGCAAGGTCGCAAGGTGAAGAACTTAAACCGAGAAATTCA 145
DB 491 CCGCCATGAAATTTTGTTCACACAAAGTCAAGGTGAAGAACTTAAACCGAGAAATTCA 550
QY 146 GCAATTCATGACCAAGATCAAAAGTACTGCTCTGACCTGGGAACTTCATGACAGTTC 205
DB 551 GCAATTCATGACCAAGATCAAAAGTACTGCTCTGACCTGGGAACTTCATGACAGTTC 610
QY 206 CAGATAAAACTCATATACGCCCGAGAGATCTTCTTGCATTAGGCTCAGCTTGAAGCTCAG 265
DB 611 CAGATAAAACTCATATACGCCCGAGAGATCTTCTTGCATTAGGCTCAGCTTGAAGCTCAG 670
QY 266 CCTCTGCGGAGAAAGAGAGTCCGATTCCTCTGCGGAGTCTCTAAAGGAGATTGTCCTCT 325
DB 671 CCTCTGCGGAGAAAGAGAGTCCGATTCCTCTGCGGAGTCTCTAAAGGAGATTGTCCTCT 730
QY 326 ACTGTGACAAAGGTAAGAAGCAAGTCAATCCCTTCAGCTGGAAGAGAGAACTCA 385
DB 731 ACTGTGACAAAGGTAAGAAGCAAGTCAATCCCTTCAGCTGGAAGAGAGAACTCA 790
QY 386 TGAAGCTGGCTGCGCAAAAGAGATTCAGACGCGGCCCTTCATCTTTATAGGCTCAGG 445
DB 791 TGAAGCTGGCTGCGCAAAAGAGATTCAGACGCGGCCCTTCATCTTTATAGGCTCAGG 850
QY 446 TGGGCTCTTGGAACATGCTGAGTCCGCGGCTCAACCCCGAGATGTTTCATCTGACCTCCT 505
DB 851 TGGGCTCTTGGAACATGCTGAGTCCGCGGCTCAACCCCGAGATGTTTCATCTGACCTCCT 910

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QY 506 GCAATTTGTAATGAGCTGTGTGGGATGACAGATTAATTTGAGAACAGAAACATTTGAT 565
DB 911 GCAATTTGTAATGAGCTGTGTGGGATGACAGATTAATTTGAGAACAGAAACATTTGAT 970
QY 566 TTTTCATTTCAACCAAGTTTGCAAAAGCTGAAATGAGCCCAAGTGAAGTTCAGGATTTGGGTA 625
DB 971 TTTTCATTTCAACCAAGTTTGCAAAAGCTGAAATGAGCCCAAGTGAAGTTCAGGATTTAGGAA 1030
QY 626 C 626
DB 1031 C 1031

RESULT 5
ADN05011
ID ADN05011 standard; cDNA; 793 BP.
XX AC ADN05011;
XX DT 01-JUL-2004 (first entry)
XX DE Antipsoriatic cDNA sequence #720.
XX KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
XX OS Homo sapiens.
XX PN WO2004028479-A2.
XX PD 08-APR-2004.
XX PF 25-SEP-2003; 2003WO-US030907.
XX PR 25-SEP-2002; 2002US-0414006P.
XX PA (GENTH ) GENENTECH INC.
XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX PI Wu TD;
XX DR WPI; 2004-305105/28.
XX DR P-PSDB; ADN05012.
XX PT New PRO-nucleic acid or polypeptide, useful for preparing a
XX PT pharmaceutical composition for diagnosing or treating psoriasis in a
XX PT mammal.
XX PS Claim 1; SEQ ID NO 1405; 3069pp; English.
XX CC The invention relates to novel polynucleotide and polypeptides for
XX CC treating psoriasis or a sequence having at least 80% identity to the
XX CC above sequences. The nucleic acid is useful for preparing a composition
XX CC for diagnosing or treating psoriasis in a mammal. This sequence
XX CC corresponds to one of the polynucleotides of the invention.
XX SQ Sequence 793 BP; 241 A; 188 C; 182 G; 182 T; 0 U; 0 Other;

Query Match 79.5%; Score 516.8; DB 12; Length 793;
Best Local Similarity 98.7%; Pred. No. 4,5e-159;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 99 TCTTTGACAGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTGAGATTGATGACCA 158
DB 183 TCTTTGACAGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTGAGATTGATGACCA 242
QY 159 GGATCACAAAGTACTGCTCTGGAATCTGGGAATCTCATAGCAAGTTCAGATAAAACTA 218
DB 243 GGATCACAAAGTACTGCTCTGGAATCTGGGAATCTCATAGCAAGTTCAGATAAAACTA 302
QY 219 CATAGCCCAAGAGATCTTTTGTGATTAAGCTTCATCTTGAAGCTCAGCTTCGCGAGAA 278
DB 303 CATAGCCCAAGAGATCTTTTGTGATTAAGCTTCATCTTGAAGCTCAGCTTCGCGAGAA 362

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QY AGGAAGTCGATTCCTCTGGGGGTCTTAAGGGAGTTTGTCTACTGTGACAAGA 338  
 DB 363 AGGAAGTCGATTCCTCTGGGGGTCTTAAGGGAGTTTGTCTACTGTGACAAGA 422  
 QY 339 TAAAGACAAGTCATCCATCCCTTCAAGTGAAGAAAGAACTGATGAAGCTGCTGC 398  
 DB 423 TAAAGACAAGTCATCCATCCCTTCAAGTGAAGAAAGAACTGATGAAGCTGCTGC 482  
 QY 399 CCAAAAGATACGACGCGCGCTTCAATCTTTTATAGGGCTCAGTGGCTCCCTGGA 458  
 DB 483 CCAAAAGATACGACGCGCGCTTCAATCTTTTATAGGGCTCAGTGGCTCCCTGGA 542  
 QY 459 CATGCTGAGTGGCGGCTCACCCCGAGTGTTCATCTGCACCTCTGCAATTTGATGA 518  
 DB 543 CATGCTGAGTGGCGGCTCACCCCGAGTGTTCATCTGCACCTCTGCAATTTGATGA 602  
 QY 519 GCCTGTTGGGGTGACAGATTAATTGAGAACAGAAACATTTGAAATTTTCAATTTCAACC 578  
 DB 603 GCCTGTTGGGGTGACAGATTAATTGAGAACAGAAACATTTGAAATTTTCAATTTCAACC 662  
 QY 579 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAAGGTTAC 626  
 DB 663 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAAGGTTAC 710  
 RESULT 6  
 AAC66727  
 ID AAC66727 standard; cDNA; 802 BP.  
 XX AAC66727;  
 AC  
 XX  
 DT 13-FEB-2001 (first entry)  
 XX  
 DE Human interleukin-1 homologue IL-1H4 coding sequence.  
 XX  
 XX Human; interleukin-1 homologue; IL-1H4; inflammation; septicemia;  
 KW autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;  
 KW transplant rejection; graft versus host disease; infection; stroke;  
 KW ischaemia; acute respiratory disease; allergy; asthma; restenosis;  
 KW brain injury; AIDS; bone disease; osteoporosis; cancer;  
 KW congestive heart failure; atherosclerosis; Alzheimer's disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200063226-A1.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 14-APR-2000; 2000WO-US010207.  
 XX  
 PR 16-APR-1999; 99US-00293625.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Young PR, McDonnell PC;  
 XX  
 DR WPI: 2000-687155/67.  
 XX  
 DR P-PSDB; AAB28266.  
 XX  
 PT Interleukin-1 homolog useful for treating conditions such as chronic and  
 PT acute inflammation, septicemia, autoimmune diseases ischemia, acute  
 PT respiratory disease, allergies, and asthma.  
 XX  
 PS Claim 2; Page 28; 30pp; English.  
 CC The present sequence is the coding sequence for human interleukin-1  
 CC homologue (IL-1H4). IL-1H4 is useful for treating conditions such as  
 CC chronic and acute inflammation, septicemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis, and arthritis), transplant  
 CC rejection, graft versus host disease, infection, stroke, ischaemia, acute  
 CC respiratory disease, allergies, asthma, restenosis, brain injury, AIDS,  
 CC bone diseases (e.g. osteoporosis), cancer, congestive heart failure,

CC atherosclerosis, and Alzheimer's disease, related to either an excess of,  
 CC or an under-expression of, IL-1H4 polypeptide activity  
 XX  
 SQ Sequence 802 BP; 243 A; 190 C; 185 G; 184 T; 0 U; 0 Other;  
 Query Match 79.5%; Score 516.8; DB 3; Length 802;  
 Best Local Similarity 98.7%; Pred. No. 4,5e-159;  
 Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 99 TCTTTGACAGGTCCCAAGGTGAAGACTTAACCCGAAAGAAATTCAGATTCATGACCA 158  
 DB 192 TCTTCAACAGATTCACAAAGGTGAAGACTTAACCCGAAAGAAATTCAGATTCATGACCA 251  
 QY 159 GGATCAACAAGTACGTCTGCTGAGCTCTGGGAATCTCATAGAGTTCAGATTAACCTA 218  
 DB 252 GGATCAACAAGTACGTCTGCTGAGCTCTGGGAATCTCATAGAGTTCAGATTAACCTA 311  
 QY 219 CATAGCCCAAGATCTTCTTGTGCAATTAAGCTCATCTTGAAGCTGAGCTCTGCGAGAA 278  
 DB 312 CATAGCCCAAGATCTTCTTGTGCAATTAAGCTCATCTTGAAGCTGAGCTCTGCGAGAA 371  
 QY 279 AGGAAGTCGATTCCTCTGGGGGTCTTAAGGGAGTTTGTCTACTGTGACAAGA 338  
 DB 372 AGGAAGTCGATTCCTCTGGGGGTCTTAAGGGAGTTTGTCTACTGTGACAAGA 431  
 QY 339 TAAAGACAAGTCATCCATCCCTTCAAGTGAAGAAAGAACTGATGAAGCTGCTGC 398  
 DB 432 TAAAGACAAGTCATCCATCCCTTCAAGTGAAGAAAGAACTGATGAAGCTGCTGC 491  
 QY 399 CCAAAAGATACGACGCGCGCTTCAATCTTTTATAGGGCTCAGTGGCTCCCTGGA 458  
 DB 492 CCAAAAGATACGACGCGCGCTTCAATCTTTTATAGGGCTCAGTGGCTCCCTGGA 551  
 QY 459 CATGCTGAGTGGCGGCTCACCCCGAGTGTTCATCTGCACCTCTGCAATTTGATGA 518  
 DB 552 CATGCTGAGTGGCGGCTCACCCCGAGTGTTCATCTGCACCTCTGCAATTTGATGA 611  
 QY 519 GCCTGTTGGGGTGACAGATTAATTGAGAACAGAAACATTTGAAATTTTCAATTTCAACC 578  
 DB 612 GCCTGTTGGGGTGACAGATTAATTGAGAACAGAAACATTTGAAATTTTCAATTTCAACC 671  
 QY 579 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAAGGTTAC 626  
 DB 672 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAAGGTTAC 719  
 RESULT 7  
 AAF84120  
 ID AAF84120 standard; cDNA; 802 BP.  
 XX  
 XX AAF84120;  
 AC  
 XX  
 DT 22-AUG-2001 (first entry)  
 XX  
 DE Interleukin-1 homologue (IL-1H4) polypeptide encoding cDNA.  
 XX  
 XX Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;  
 KW immunosuppressive; antipsoriatic; antiarthritic; cytostatic; antiHIV;  
 KW cerebroprotective; antiasthmatic; vasotropic; vulnary; osteopathic;  
 KW immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;  
 KW gene therapy; vaccine; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT CDS Location/Qualifiers  
 FT /tag= a  
 FT /product= "IL-1H4"  
 FT sig\_peptide 58..117  
 FT /\*tag= b  
 FT mat\_peptide 118..711  
 FT /\*tag= c



Best Local Similarity 98.7%; Pred. No. 4.6e-159;  
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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OY 99 TCTTTCAGAGGTCCTCAAGTGAAGAACTTAAACCCGAGAAATTCAGATTCATGACCA 158
DB 207 TGTTCACACAAAGTCCAAAGGTGAAGACTTAAACCCGAGAAATTCAGATTCATGACCA 266
OY 159 GGATCAACAAAGTACTGCTCTGAGACTCTGGAATCTCATAGCAGTTCAGATTAATACTA 218
DB 267 GGATCAACAAAGTACTGCTCTGAGACTCTGGAATCTCATAGCAGTTCAGATTAATACTA 326
OY 219 CATAGCCCAAGAGATCTTCTTGATTAAGCTTCATCTTGAGCTCAGCTCTGCGAGAA 278
DB 327 CATAGCCCAAGAGATCTTCTTGATTAAGCTTCATCTTGAGCTCAGCTCTGCGAGAA 386
OY 279 AGGAAGTCCGATTCCTGCGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGA 338
DB 387 AGGAAGTCCGATTCCTGCGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGA 446
OY 339 TAAAGGACAAAGTCAATCCCTTCAGCTGAAGAGAACTGATGAAGCTGCTGC 398
DB 447 TAAAGGACAAAGTCAATCCCTTCAGCTGAAGAGAACTGATGAAGCTGCTGC 506
OY 399 CCAAAAGGATCAGACGCGCGCTTCATCTTTATAGGCTCAGGTGCGCTCTGGA 458
DB 507 CCAAAAGGATCAGACGCGCGCTTCATCTTTATAGGCTCAGGTGCGCTCTGGA 566
OY 459 CATGCTGAGTGGCGGCTCAGCCCGAGGTTCATCTGACCTCTGCAATTTGATGA 518
DB 567 CATGCTGAGTGGCGGCTCAGCCCGAGGTTCATCTGACCTCTGCAATTTGATGA 626
OY 519 GCCTGTGGGGTGACAGATTAATTTGAGAAAGAAACATTTGAATTTTCAATTCAC 578
DB 627 GCCTGTGGGGTGACAGATTAATTTGAGAAAGAAACATTTGAATTTTCAATTCAC 686
OY 579 AGTTTGCAAGCTGAATGAGCCCGAGGTGAGCGGATTTAGGTTAC 626
DB 687 AGTTTGCAAGCTGAATGAGCCCGAGGTGAGCGGATTTAGGTTAC 734
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## RESULT 9

AAD00210  
ID AAD00210 standard; cDNA; 1600 BP.

AC AAD00210;

XX 05-SEP-2000 (first entry)

DE Human zilla4 cDNA.

XX Human interleukin-1, IL-1, zilla4 protein; inflammation; arthritis;  
XX psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;  
XX anaemia; inflammatory bowel disease; acute neuropathology; shock;  
XX chronic neuropathology; respiratory disease syndrome; restenosis;  
XX acquired immune deficiency syndrome; AIDS; anti-inflammatory; cyclostatic;  
XX anti-arthritis; anti-psoriasis; antibacterial; immunosuppressive;  
XX anti-anaemic; neuroprotective; vasotropic;  
XX anti-human immunodeficiency virus; HIV; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Key 647..1503

XX Key CDS /tag= a

XX Key WO200024899-A2.

XX Key 04-MAY-2000.

XX Key 27-OCT-1999; 99WO-US025038.

XX Key 27-OCT-1998; 98US-00179614.

XX (ZYMO) ZYMOGENETICS INC.

PI West RR, Sheppard PO, Gao Z;

XX MPI; 2000-350740/30.

DR P-PSDB; AAY70927.

PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for  
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host  
PT disease, leukaemia.

XX Example 2; Page 61-63; 88pp; English.

CC The present cDNA sequence encodes human interleukin (IL)-1 homolog zilla4  
CC protein. This cDNA was cloned from a human foetal lung cDNA library. The  
CC zilla4 proteins modulate inflammation and other immunological processes  
CC and are therefore useful for treatment of arthritis, psoriasis, septic  
CC shock, graft-versus-host disease and leukaemia. Other diseases that may  
CC be modulated by zilla4 proteins include cancer, anaemia, inflammatory  
CC bowel disease, acute and chronic neuropathologies, shock, respiratory  
CC disease syndrome, restenosis and acquired immune deficiency syndrome  
XX

SQ Sequence 1600 BP; 481 A; 356 C; 378 G; 385 T; 0 U; 0 Other;

Query Match 79.5%; Score 516.8; DB 3; Length 1600;

Best Local Similarity 98.7%; Pred. No. 6.6e-159;  
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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OY 99 TCTTTCAGAGGTCCTCAAGTGAAGAACTTAAACCCGAGAAATTCAGATTCATGACCA 158
DB 981 TCTTTCAGAGGTCCTCAAGTGAAGAACTTAAACCCGAGAAATTCAGATTCATGACCA 1040
OY 159 GGATCAACAAAGTACTGCTCTGAGACTCTGGAATCTCATAGCAGTTCAGATTAATACTA 218
DB 1041 GGATCAACAAAGTACTGCTCTGAGACTCTGGAATCTCATAGCAGTTCAGATTAATACTA 1100
OY 219 CATAGCCCAAGAGATCTTCTTGATTAAGCTTCATCTTGAGCTCAGCTCTGCGAGAA 278
DB 1101 CATAGCCCAAGAGATCTTCTTGATTAAGCTTCATCTTGAGCTCAGCTCTGCGAGAA 1160
OY 279 AGGAAGTCCGATTCCTGCGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGA 338
DB 1161 AGGAAGTCCGATTCCTGCGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGA 1220
OY 339 TAAAGGACAAAGTCAATCCCTTCAGCTGAAGAGAACTGATGAAGCTGCTGC 398
DB 1221 TAAAGGACAAAGTCAATCCCTTCAGCTGAAGAGAACTGATGAAGCTGCTGC 1280
OY 399 CCAAAAGGATCAGACGCGCGCTTCATCTTTATAGGCTCAGGTGCGCTCTGGA 458
DB 1281 CCAAAAGGATCAGACGCGCGCTTCATCTTTATAGGCTCAGGTGCGCTCTGGA 1340
OY 459 CATGCTGAGTGGCGGCTCAGCCCGAGGTTCATCTGACCTCTGCAATTTGATGA 518
DB 1341 CATGCTGAGTGGCGGCTCAGCCCGAGGTTCATCTGACCTCTGCAATTTGATGA 1400
OY 519 GCCTGTGGGGTGACAGATTAATTTGAGAAAGAAACATTTGAATTTTCAATTCAC 578
DB 1401 GCCTGTGGGGTGACAGATTAATTTGAGAAAGAAACATTTGAATTTTCAATTCAC 1460
OY 579 AGTTTGCAAGCTGAATGAGCCCGAGGTGAGCGGATTTAGGTTAC 626
DB 1461 AGTTTGCAAGCTGAATGAGCCCGAGGTGAGCGGATTTAGGTTAC 1508
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## RESULT 10

ADH89066  
ID ADH89066 standard; DNA; 1600 BP.

XX ADH89066;

XX 22-APR-2004 (first entry)

XX	DE	DNA encoding human z11a4 polypeptide.
XX	KW	Human; interleukin-1 homologue; IL-1; z11a4; immune response;
XX	KW	inflammatory disease; cancer; anaemia; immunomodulator; antiinflammatory;
XX	KW	cytostatic; antianaemic; chromosome 2; gene; ds.
XX	OS	Homo sapiens.
XX	PH	Key
XX	FT	CDS
XX	FT	Location/Qualifiers
XX	FT	847..1503
XX	FT	/*tag= a
XX	FT	/product= "z11a4"
PN	US	2003148467-A1.
XX	XX	
XX	PD	07-AUG-2003.
XX	PF	22-NOV-2002; 2002US-00302554.
XX	PR	27-OCT-1998; 98US-0105824P.
XX	PR	27-OCT-1999; 99US-00428118.
XX	PA	(Zymo ) ZYMOGENETICS INC.
XX	PI	West RR, Sheppard PO, Gao Z;
XX	DR	WPI; 2003-897576/82.
XX	DR	P-PSDB; ADH89067.
XX	PT	New interleukin-1 homologue z11a4 protein, useful for modulating an immune
XX	PT	response and for treating diseases, e.g., inflammatory diseases, cancer
XX	PT	or anemia.
XX	PS	Example 2; SEQ ID NO 1; 44p; English.
XX	CC	The present invention relates to the isolation of human interleukin-1 (IL
XX	CC	-1) homologues designated z11a4, and the polynucleotide sequences that
XX	CC	encode them. The gene encoding human z11a4 is located on chromosome 2.
XX	CC	Also disclosed is a method of making these proteins and a method of
XX	CC	modulating an immune response. The proteins are useful for treating
XX	CC	diseases such as inflammatory diseases, cancer, and anaemia. The present
XX	CC	sequence encodes human z11a4.
XX	SQ	Sequence 1600 BP; 481 A; 356 C; 378 G; 385 T; 0 U; 0 Other;
QY	Query Match	79.5%; Score 516.8; DB 10; Length 1600;
QY	Best Local Similarity	98.7%; Pred. No. 6.6e-159;
QY	Matches 521; Conservative	0; Mismatches 7; Indels 0; Gaps 0;
QY	99	TCCTTTCGAGAGGTCCAAAGGTGAAGACTTAAACCGGAAGAAATTCAGCATTCATGACCA 158
DB	981	TGTTTCACACAGTCGCAAGGTGAAGACTTAAACCGGAAGAAATTCAGCATTCATGACCA 1040
QY	159	GGATTCACAAAGTATCTGCTCTGGAGCTCTGGAGATCTCATAGCAGTTCAGATTAATACTA 218
DB	1041	GGATTCACAAAGTATCTGCTCTGGAGCTCTGGAGATCTCATAGCAGTTCAGATTAATACTA 1100
QY	219	CATAGCGCCGAGAGATCTTCTTGACATTAAGCTCATCTTGAAGCTCAGCTTCGGAGAA 278
DB	1101	CATAGCGCCGAGAGATCTTCTTGACATTAAGCTCATCTTGAAGCTCAGCTTCGGAGAA 1160
QY	279	AGGAAGTCGATCTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAGGA 338
DB	1161	AGGAAGTCGATCTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAGGA 1220
QY	339	TAAAGGACAAAGTCATCCATCCCTTAGCTGGAAGAGGAAGTGAAGAGTGGCTGC 398
DB	1221	TAAAGGACAAAGTCATCCATCCCTTAGCTGGAAGAGGAAGTGAAGAGTGGCTGC 1280
QY	399	CCAAAAGGATCGACAGCGCGGCTTCATCTTTTAAAGGCTCAGGTGGCTCCTGGAA 458
DB	1281	CCAAAAGGATCGACAGCGCGGCTTCATCTTTTAAAGGCTCAGGTGGCTCCTGGAA 1340

QY	459	CATGCTGAGTCGGGGGCTCA	CCCCGGANGGTATTCGCAACCTCCTGCAATTGTAA	511
Db	1341	CATGCTGAGTCGGGGGCTCA	CCCCGGATGGTTCATCTCGACCTCTGCAATTGTAA	1401
QY	519	GCCTGTTGGGGGTGACAGAT	TAATTGAGAACAGAAACACATTTGATTTTCATTTCAACC	578
Db	1401	GCGCTGTTGGGGGTGACAGAT	TAATTGAGAACAGAAACACATTTGATTTTCATTTCAACC	1461
QY	579	AGTTTGCAAGCTGAAATGAG	CCCCCAGTGAAGGTCAAGCATTTAGGGTAC	626
Db	1461	AGTTTGCAAGCTGAAATGAG	CCCCCAGTGAAGGTCAAGCATTTAGGAAC	1508
RESULT 11				
AAA27918	ID	AAA27918	standard; cDNA, 579 BP.	
XX	XX	AAA27918;		
XX	AC	12-SEP-2000	(first entry)	
XX	DT			
XX	DE		Human interleukin-1 zeta cDNA coding region.	
XX	XX		Interleukin-1 zeta; IL-1 zeta; human; chromosome 2; gene therapy;	
KW	glaucoma; ectodermal dysplasia; winkly skin syndrome;			
KM	insulin-dependent diabetes mellitus; leukaemia; lymphoma;			
KW	tibial muscular dystrophy; ss.			
XX				
OS	Homo sapiens.			
PN	WO200036108-A2.			
XX				
PD	22-JUN-2000.			
XX				
PF	14-DEC-1999;	99WO-US029549.		
PR	14-DEC-1998;	98US-0112163P.		
PR	10-NOV-1999;	99US-0164675P.		
XX				
PA	(IMMV ) IMMUNEX CORP.			
PI	Sims JE, Smith DE, Born TL;			
DR	WPI; 2000-442387/38.			
DR	P-PSDB; AAY95297.			
XX				
PT	Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants			
PT	TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for			
PT	identifying genes associated with diseases such as glaucoma, and insulin-			
PT	dependent diabetes mellitus.			
PS	Claim 1(a); Page 8; 87bp; English.			
XX				
CC	The present sequence is that of the coding region of cDNA encoding human			
CC	interleukin-1 zeta (IL-1 zeta, see AAY95297), a member of the IL-1			
CC	family. The sequence was deduced from EST IMAGB clone 1628791, which			
CC	encoded a partial open reading frame, and from additional sequences			
CC	obtained from PCR and 5' RACE reactions. IL-1 zeta mRNA is generated from			
CC	exons 3-6 of the IL-1 zeta locus. The mRNA is expressed most strongly in			
CC	the testis, prostate, colon, brain, placenta, lung, foetal liver and			
CC	lymph node. The invention is directed to novel, purified and isolated IL-			
CC	1 zeta, IL-1 zeta splice variants and Xrec2 polypeptides (see AAY95297-			
CC	301), the nucleic acids (see AAA27918-22) encoding such polypeptides,			
CC	processes for production of recombinant forms of such polypeptides, and			
CC	their uses. IL-1 zeta nucleic acids are used to: to express IL-1 zeta			
CC	polypeptides; as probes to identify nucleic acids encoding proteins of			
CC	the IL-1 ligand family; to identify human chromosome 2; to map genes on			
CC	chromosome 2; to identify genes associated with diseases, syndromes, or			
CC	other conditions associated with chromosome 2, such as glaucoma,			
CC	ectodermal dysplasia, insulin-dependent diabetes mellitus, winkly skin			
CC	syndrome, T-cell leukaemia or lymphoma, and tibial muscular dystrophy; as			
CC	single-stranded sense or antisense oligonucleotides to inhibit expression			



CC of IL-1 zeta polypeptides, to help detect defective genes in an  
XX individual, and for gene therapy

CC Sequence 579 BP; 173 A; 129 C; 146 G; 131 T; 0 U; 0 Other;

Query Match 79.4%; Score 516; DB 3; Length 579;  
Best Local Similarity 100.0%; Pred. No. 6.9e-159;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 106 AGAGGTCCTAAAGTGAAGTAACTTAACCCGAGAAATTCAGCTTATGACCGAGATCAC 165
DB 64 AGAGGTCCTAAAGTGAAGTAACTTAACCCGAGAAATTCAGCTTATGACCGAGATCAC 123
OY 166 AAAGTACTGCTGCTGAGCTCTGGGAATCTCATAGCAGTTCCAGATTAACATACATCCG 225
DB 124 AAAGTACTGCTGCTGAGCTCTGGGAATCTCATAGCAGTTCCAGATTAACATACATCCG 183
OY 226 CCAGAGATCTTCTTTGATTAAGCTTCATCCTTGAAGCTCCTGCGGAGAAAGGAGT 285
DB 184 CCAGAGATCTTCTTTGATTAAGCTTCATCCTTGAAGCTCCTGCGGAGAAAGGAGT 243
OY 286 CGATTTCTCTGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGATTAAGGA 345
DB 244 CGATTTCTCTGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGATTAAGGA 303
OY 346 CAAAGTCATCCATCCCTTCACTGAGTGAAGAGAACTGATGAAGCTGGCTGCCAAAAG 405
DB 304 CAAAGTCATCCATCCCTTCACTGAGTGAAGAGAACTGATGAAGCTGGCTGCCAAAAG 363
OY 406 GAATCAGACGCGCGCCCTTCACTTATTAAGGCTCAGTGGGCTCTGGAACATGCTG 465
DB 364 GAATCAGACGCGCGCCCTTCACTTATTAAGGCTCAGTGGGCTCTGGAACATGCTG 423
OY 466 GAGTGGGGCTCACCCTGGATGTTTCACTGCACTCTGCAATTTGATAGCTGTT 525
DB 424 GAGTGGGGCTCACCCTGGATGTTTCACTGCACTCTGCAATTTGATAGCTGTT 483
OY 526 GGGGTGACAGATTAATTTGAGAACAGAAACAATTGAATTTTCAATTCACAGTTTGC 585
DB 484 GGGGTGACAGATTAATTTGAGAACAGAAACAATTGAATTTTCAATTCACAGTTTGC 543
OY 586 AAAGCTGAATATGAGCCCGAGTGAAGTCAAGCGATTAG 621
DB 544 AAAGCTGAATATGAGCCCGAGTGAAGTCAAGCGATTAG 579
```

RESULT 12  
ADN05879  
ID ADN05879 standard; cDNA; 579 BP.

XX AC ADN05879;  
XX DT 01-JUL-2004 (first entry)

DE Antipsoriatic cDNA sequence #1171.

KM ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.

XX OS Homo sapiens.

XX PN W02004028479-A2.

XX PD 08-APR-2004.

XX PF 25-SEP-2003; 2003WO-US030907.

XX PR 25-SEP-2002; 2002US-0414006P.

XX PA (GETH ) GENENTECH INC.

XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
XX Wu TD;

DR WPI; 2004-305105/28.  
XX P-PSDB; ADN05880.

PT New PRO nucleic acid or polypeptide, useful for preparing a  
XX pharmaceutical composition for diagnosing or treating psoriasis in a  
XX mammal.

PS Claim 1; SEQ ID NO 2274; 3069pp; English.

CC The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polynucleotides of the invention.

XX Sequence 579 BP; 173 A; 129 C; 146 G; 131 T; 0 U; 0 Other;

Query Match 79.4%; Score 516; DB 12; Length 579;  
Best Local Similarity 100.0%; Pred. No. 6.9e-159;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 106 AGAGTCCAAAGTGAAGTAACTTAACCCGAGAAATTCAGCTTATGACCGAGATCAC 165
DB 64 AGAGTCCAAAGTGAAGTAACTTAACCCGAGAAATTCAGCTTATGACCGAGATCAC 123
OY 166 AAAGTACTGCTGCTGAGCTCTGGGAATCTCATAGCAGTTCCAGATTAACATACATCCG 225
DB 124 AAAGTACTGCTGCTGAGCTCTGGGAATCTCATAGCAGTTCCAGATTAACATACATCCG 183
OY 226 CCAGAGATCTTCTTTGATTAAGCTTCATCCTTGAAGCTCCTGCGGAGAAAGGAGT 285
DB 184 CCAGAGATCTTCTTTGATTAAGCTTCATCCTTGAAGCTCCTGCGGAGAAAGGAGT 243
OY 286 CGATTTCTCTGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGATTAAGGA 345
DB 244 CGATTTCTCTGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGATTAAGGA 303
OY 346 CAAAGTCATCCATCCCTTCACTGAGTGAAGAGAACTGATGAAGCTGGCTGCCAAAAG 405
DB 304 CAAAGTCATCCATCCCTTCACTGAGTGAAGAGAACTGATGAAGCTGGCTGCCAAAAG 363
OY 406 GAATCAGACGCGCGCCCTTCACTTATTAAGGCTCAGTGGGCTCTGGAACATGCTG 465
DB 364 GAATCAGACGCGCGCCCTTCACTTATTAAGGCTCAGTGGGCTCTGGAACATGCTG 423
OY 466 GAGTGGGGCTCACCCTGGATGTTTCACTGCACTCTGCAATTTGATAGCTGTT 525
DB 424 GAGTGGGGCTCACCCTGGATGTTTCACTGCACTCTGCAATTTGATAGCTGTT 483
OY 526 GGGGTGACAGATTAATTTGAGAACAGAAACAATTGAATTTTCAATTCACAGTTTGC 585
DB 484 GGGGTGACAGATTAATTTGAGAACAGAAACAATTGAATTTTCAATTCACAGTTTGC 543
OY 586 AAAGCTGAATATGAGCCCGAGTGAAGTCAAGCGATTAG 621
DB 544 AAAGCTGAATATGAGCCCGAGTGAAGTCAAGCGATTAG 579
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RESULT 13  
AAA08513  
ID AAA08513 standard; DNA; 657 BP.

XX AC AAA08513;

XX DT 19-JUL-2000 (first entry)

DE Primate interleukin-1 like (IL-1-zeta) alternative coding sequence.

XX KW Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;  
XX hypoglycemia; plasma iron; plasma zinc; acute liver response;  
XX plasma copper; ss.

XX OS Mammalia.

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XX WO200017363-A2.
PN |||
XX 30-MAR-2000.
PD |||
XX 17-SEP-1999; 99WO-US020868.
XX 18-SEP-1998; 98US-00156966.
XX (SCHE ) SCHERING CORP.
XX Timans JC;
XX WPI; 2000-283588/24.
DR P-PSDB; AAY91885.
XX New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
PT for diagnostic and therapeutic purposes, comprises a 128 amino acid
PT sequence.
XX
XX Disclosure; Page 102-103; 110pp; English.
XX
XX The present sequence encodes a primate interleukin-1 like molecule,
CC designated IL-1-zeta. It is an alternative sequence to AAA08512, perhaps
CC an allelic variant. The specification claims an isolated or recombinant
CC polypeptide that: (a) specifically binds polyclonal antibodies generated
CC against at least a 12 consecutive amino acid segment of IL-1-zeta (see
CC AAY91884) or its allelic variant (see AAY91885); and (b) comprises at
CC least one sequence selected from: AAY91886-903 or AAY91904-06. The
CC preferred 12 consecutive amino acid segment is chosen from AAY91907-18 or
CC AAY91919-21. IL-1-zeta is likely to play a role in systemic inflammatory
CC reactions, such as fever, hypoglycemia, reduced plasma iron and zinc, the
CC acute response of the liver, and increase plasma copper. IL-1-zeta
CC binding compounds (comprising antigen binding sites) and IL-1-zeta
CC polypeptides are also useful for both diagnostic and therapeutic purposes
CC
XX Sequence 657 BP; 184 A; 158 C; 166 G; 149 T; 0 U; 0 Other;
SQ
Query Match 79.3%; Score 515.2; DB 3; Length 657;
Best Local Similarity 97.6%; Pred. No. 1.4e-158;
Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
XX 86 CCGCGAATTCAGCTCTTTCGAGAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCA 145
DB |||
XX 122 CCGCCATGAATTTGTTTCACACAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCA 181
DB |||
XX 146 GCATTCATGACCGAGATCAACAAAGTACTGCTCTGACCTCTGGGAATTCATGCACTTC 205
DB |||
XX 182 GCAATTCATGACCGAGATCAACAAAGTACTGCTCTGACCTCTGGGAATTCATGCACTTC 241
DB |||
XX 206 CAGATTAATACTACATACGCGCCGAGATCTCTTCGATTAAGCTCATGCTGAGCTCAG 265
DB |||
XX 242 CAGATTAATACTACATACGCGCCGAGATCTCTTCGATTAAGCTCATGCTGAGCTCAG 301
DB |||
XX 266 CCTCTCGGAGAAAGAGTCCGATTCCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCT 325
DB |||
XX 302 CCTCTCGGAGAAAGAGTCCGATTCCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCT 361
DB |||
XX 326 ACTGTGACAGAGTAAGAACAAGTATCATCTCTTCAGCTGAGAAAGAGAACTGA 385
DB |||
XX 362 ACTGTGACAGAGTAAGAACAAGTATCATCTCTTCAGCTGAGAAAGAGAACTGA 421
DB |||
XX 386 TGAAGTGTGCTGCCAAAGAGATCAGACGCGGCTTCATCTTTTAAGGGCTCAG 445
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XX 422 TGAAGTGTGCTGCCAAAGAGATCAGACGCGGCTTCATCTTTTAAGGGCTCAG 481
DB |||
XX 446 TGGGCTCTTGGAACATGCTGAGTCCGCGGCTCACCCCGAGATGTTTCATGCACTCTCT 505
DB |||
XX 482 TGGGCTCTTGGAACATGCTGAGTCCGCGGCTCACCCCGAGATGTTTCATGCACTCTCT 541
DB |||
XX 506 GCAATTTGTAATGAGCTGTTGGGGTGAACAGATAAATTTGAGAACAGAGAAACACATTTGAAT 565
DB |||
XX 542 GCAATTTGTAATGAGCTGTTGGGGTGAACAGATAAATTTGAGAACAGAGAAACACATTTGAAT 601

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XX 566 TTTTCATTTCAACCAAGTTTGCAAGCTGAATGAGCCCGAGTGAAGCGATTAG 621
DB |||
XX 602 TTTTCATTTCAACCAAGTTTGCAAGCTGAATGAGCCCGAGTGAAGCGATTAG 657
DB |||
RESULT 14
ADJ88305
ID ADJ88305 strand; DNA; 657 BP.
XX
XX ADJ88305;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human interleukin-1zeta DNA variant.
XX
XX Interleukin-1zeta, gene therapy; immune system; haematopoietic cell;
KW inflammatory disorder; infection; allergy; cancer; human; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 1..657
FT /*tag= a
FT /product= "Human IL-1zeta variant"
XX
XX US6680380-B1.
XX
XX 20-JAN-2004.
XX
XX 17-SEP-1999; 99US-00398412.
XX
XX 18-SEP-1998; 98US-0100948P.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Timans JC;
XX
XX WPI; 2004-189656/18.
DR P-PSDB; ADJ88306.
XX
XX New nucleic acid molecules encoding mammalian interleukin-1 polypeptides,
PT useful for diagnosing, preventing or treating diseases associated with
PT abnormal expression of interleukin, e.g. inflammation, infection or
PT cancer.
XX
XX Claim 1, SEQ ID NO 3; 36pp; English.
XX
XX The invention relates to an isolated or recombinant nucleic acid encoding
CC interleukin-1zeta polypeptide. The invention is useful in gene therapy.
CC The composition and methods are useful in diagnosing or treating
CC degenerative or abnormal conditions which directly or indirectly involve
CC development, differentiation or function, e.g. of the immune system
CC and/or haematopoietic cells. The invention may also be used for
CC preventing or treating other diseases or disorders associated with
CC abnormal expression or triggering of responses to the interleukin, such as
CC inflammatory disorders, infection, allergies or cancer. The present
CC sequence is human interleukin-1zeta DNA variant.
XX
XX Sequence 657 BP; 184 A; 158 C; 166 G; 149 T; 0 U; 0 Other;
SQ
Query Match 79.3%; Score 515.2; DB 12; Length 657;
Best Local Similarity 97.6%; Pred. No. 1.4e-158;
Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
XX 86 CCGCGAATTCAGCTCTTTCGAGAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCA 145
DB |||
XX 122 CCGCCATGAATTTGTTTCACACAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCA 181
DB |||
XX 146 GCATTCATGACCGAGATCAACAAAGTACTGCTCTGACCTCTGGGAATTCATGCACTTC 205
DB |||
XX 182 GCAATTCATGACCGAGATCAACAAAGTACTGCTCTGACCTCTGGGAATTCATGCACTTC 241

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QY 206 CAGATAAATACTACATACGCCAGAGATCTTTTGTCATTTAGGCTCATCTTGAGCTCAG 265  
 Db 242 CAGATAAATACTACATACGCCAGAGATCTTTTGTCATTTAGGCTCATCTTGAGCTCAG 301  
 QY 266 CCTCTGCGGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCT 325  
 Db 302 CCTCTGCGGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCT 361  
 QY 326 ACTGTGACAAAGATAAAGACAAAGTATCCATCCCTTGACGTGAAGAAAGAAACTGA 385  
 Db 362 ACTGTGACAAAGATAAAGACAAAGTATCCATCCCTTGACGTGAAGAAAGAAACTGA 421  
 QY 386 TGAAGCTGCTGCGCCAAAAGAAATGACACGCCGCGCTTCATCTTTATAGGGCTCAG 445  
 Db 422 TGAAGCTGCTGCGCCAAAAGAAATGACACGCCGCGCTTCATCTTTATAGGGCTCAG 481  
 QY 446 TGGGCTCTGGAACATGCTGAGTGGCGGCTCAACCCGGATGCTTCATCTGCACTCTCT 505  
 Db 482 TGGGCTCTGGAACATGCTGAGTGGCGGCTCAACCCGGATGCTTCATCTGCACTCTCT 541  
 QY 506 GCAATTGTATGAGCTGTTGGGGTGACAGATAATTTTGAACAGAGAAACATTTGAAT 565  
 Db 542 GCAATTGTATGAGCTGTTGGGGTGACAGATAATTTTGAACAGAGAAACATTTGAAT 601  
 QY 566 TTTCAATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCAATTAG 621  
 Db 602 TTTCAATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCAATTAG 657

## RESULT 15

ADL15867  
 ID ADL15867 standard; cDNA; 657 BP.

AC ADL15867;

XX 01-JUL-2004 (first entry)

DE Human interleukin 1 zeta (IL-1zeta) cDNA seqid 3.

XX antiinflammatory; interleukin 1 zeta; IL-1 zeta; immunogen;  
 KM antisera production; antibody production; anti-inflammatory; human; gene;  
 68.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 1..657  
 FT /tag= a  
 FT /product= "IL-1 zeta"  
 FT /note= "Interleukin 1 zeta"

XX US2004068099-A1.

XX 08-APR-2004.

XX 27-OCT-2003; 2003US-00695195.

XX 18-SEP-1998; 98US-0100948P.

XX 17-SEP-1999; 99US-00398412.

XX (TIMA/) TIMANS J C.

XX Timans JC;

XX WPI: 2004-304623/28.

XX P-PSDB; ADL15868.

XX Novel isolated or recombinant interleukin 1 zeta polypeptide useful as  
 PT immunogen for producing specific antibodies or for developing anti-  
 PT inflammatory therapeutics.

XX Claim 14; SEQ ID NO 3; 42pp; English.

CC The invention describes an isolated or recombinant interleukin 1 zeta  
 CC polypeptide (I) that specifically binds to polyclonal antibodies  
 CC generated against at least a 12 consecutive amino acid segment of two  
 CC fully defined sequences (S1) and (S2) having 218 amino acids as given in  
 CC the specification and comprises at least one sequence chosen from (S1)  
 CC and (S2). Also described are: a fusion protein comprising (I) or its  
 CC sequences, a detection or purification tag, including FLAG, His6 or Ig  
 CC sequence or sequence of another cytokine or chemokine; a binding compound  
 CC (II) an antigen binding site from an antibody, which specifically binds  
 CC to (I); a composition of matter comprising a sterile polypeptide (I) or  
 CC (II), (I) or (II) and a carrier such as an aqueous compound e.g., water,  
 CC saline and/or buffer, where the carrier is formulated for oral, rectal,  
 CC nasal, topical or parental administration; an isolated or recombinant  
 CC nucleic acid (III) that encodes (I) or several antigenic peptides of (S1)  
 CC or (S2); a cell (IV) transformed with (III); a method of modulating a  
 CC cell involved in an inflammatory response, by contacting the cell with an  
 CC agonist or antagonist of (I); a kit comprising a compartment of (I), (II)  
 CC or (III) and/or instructions for use or disposal of reagents in the kit;  
 CC and producing an antibody as mentioned in (II) or an antigen-antibody  
 CC complex. (I) is useful as immunogen for producing antisera or specific  
 CC antibodies or useful for developing more effective anti-inflammatory  
 CC therapeutics. This sequence encodes a human interleukin 1 zeta  
 CC polypeptide.

SQ Sequence 657 BP; 184 A; 158 C; 166 G; 149 T; 0 U; 0 Other;

Query Match 79.3%; Score 515.2; DB 12; Length 657;

Best Local Similarity 97.6%; Pred. No. 14e-158;

Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 86 CCGCAATTCAGCTCTTTGACAGAGTCCAAAGTGAAGAACTTAAACCGAAGAAATTGA 145  
 Db 122 CCGCATGAATTTTGTTCACACAGATCCAAAGTGAAGAACTTAAACCGAAGAAATTGA 181  
 QY 146 GCATTCATGACCAAGATCAAAAGTACTGCTGAGCTTGGGAATCTCATGCACTTC 205  
 Db 182 GCATTCATGACCAAGATCAAAAGTACTGCTGAGCTTGGGAATCTCATGCACTTC 241  
 QY 206 CAGATAAATACTACATACGCCAGAGATCTTTTGTCATTTAGGCTCATCTTGAGCTCAG 265  
 Db 242 CAGATAAATACTACATACGCCAGAGATCTTTTGTCATTTAGGCTCATCTTGAGCTCAG 301  
 QY 266 CCTCTGCGGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCT 325  
 Db 302 CCTCTGCGGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCT 361  
 QY 326 ACTGTGACAAAGATAAAGACAAAGTATCCATCCCTTGACGTGAAGAAAGAAACTGA 385  
 Db 362 ACTGTGACAAAGATAAAGACAAAGTATCCATCCCTTGACGTGAAGAAAGAAACTGA 421  
 QY 386 TGAAGCTGCTGCGCCAAAAGAAATGACACGCCGCGCTTCATCTTTATAGGGCTCAG 445  
 Db 422 TGAAGCTGCTGCGCCAAAAGAAATGACACGCCGCGCTTCATCTTTATAGGGCTCAG 481  
 QY 446 TGGGCTCTGGAACATGCTGAGTGGCGGCTCAACCCGGATGCTTCATCTGCACTCTCT 505  
 Db 482 TGGGCTCTGGAACATGCTGAGTGGCGGCTCAACCCGGATGCTTCATCTGCACTCTCT 541  
 QY 506 GCAATTGTATGAGCTGTTGGGGTGACAGATAATTTTGAACAGAGAAACATTTGAAT 565  
 Db 542 GCAATTGTATGAGCTGTTGGGGTGACAGATAATTTTGAACAGAGAAACATTTGAAT 601  
 QY 566 TTTCAATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCAATTAG 621  
 Db 602 TTTCAATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCAATTAG 657

Search completed: May 28, 2005, 15:38:30  
 Job time : 436 secs

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QY	Db	QY	Db
519	GCGTGTGGGGTGACGATTAATTTTGAGAAACGGAAACACATTTAAATTTTCATTTCAAC	519	GCGTGTGGGGTGACGATTAATTTTGAGAAACGGAAACACATTTAAATTTTCATTTCAAC
612	GCGTGTGGGGTGACGATTAATTTTGAGAAACGGAAACACATTTAAATTTTCATTTCAAC	612	GCGTGTGGGGTGACGATTAATTTTGAGAAACGGAAACACATTTAAATTTTCATTTCAAC
579	AGTTTGCAAAGCTGAATATGAGCCCGACGTGAGTCAAGCATTTAGGGTAC	579	AGTTTGCAAAGCTGAATATGAGCCCGACGTGAGTCAAGCATTTAGGGTAC
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RESULT 2
US-09-398-412B-3
; Sequence 3, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-12 $\alpha$ , related reage
; TITLE OF INVENTION: methods
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(654)
; OTHER INFORMATION:
; US-09-398-412B-3

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Query Match	79.3%	Score 515.2	DB 4	Length 657
Best Local Similarity	97.6%	Pred. No. 1.9e-151		
Matches 523; Conservative		0; Mismatches 13;	Indels 0;	Gaps 0

Oy	86	CCGCGAATTAGCTCTTTTGACAGGGTCCAAAGGTGAAAGACTTAAACCCGAAAGAAATTTCA	145
Db	122	CCGCCATGAATTTTGTTCACACAAAGTCCAAAGGTGAAAGACTTAAACCCGAAAGAAATTTCA	181
Oy	146	GCATTCATGACACAGATCACAAAGTACTGGTCTTGAACTTGGGAATCTCATACAGTTC	205
Db	182	GCATTCATGACACAGATCACAAAGTACTGGTCTTGAACTTGGGAATCTCATACAGTTC	241
Oy	206	CAATATAAAACTACATACAGCCACAGATTTCTTTGCAATTAAGCCATATCCCTGAGCTCAG	265
Db	242	CAATATAAAACTACATACAGCCACAGATTTCTTTGCAATTAAGCCATATCCCTGAGCTCAG	301
Oy	266	CTCTCGGAGAAAGGAAAGTCCGATTTCTCTGGGGGTCTTAAAGGGAGTTTGTCTCT	325
Db	302	CTCTCGGAGAAAGGAAAGTCCGATTTCTCTGGGGGTCTTAAAGGGAGTTTGTCTCT	361
Oy	326	ACTGTGACAAAGATTAAAGCAAAAGTCATCCCTTCACTGAAGAAAGAAACTGA	385
Db	362	ACTGTGACAAAGATTAAAGCAAAAGTCATCCCTTCACTGAAGAAAGAAACTGA	421
Oy	386	TGAAGCTGCGTCCCAAAGGAATCAGACGCGCGCCCTCATCTTTAATGAGGCTCAGG	445
Db	422	TGAAGCTGCGTCCCAAAGGAATCAGACGCGCGCCCTCATCTTTAATGAGGCTCAGG	481
Oy	446	TGGGCTCTCGGAACATGCTGAGAGTGGGGGCTCAACCCGGATGGTTATCTGACCTTCCT	505
Db	482	TGGGCTCTCGGAACATGCTGAGAGTGGGGGCTCAACCCGGATGGTTATCTGACCTTCCT	541
Oy	506	GCAATTGTATGAGCCTGTTGGGGGTGACAGATTAATTTGAGAACAGGAAACACTTGAAAT	565
Db	542	GCAATTGTATGAGCCTGTTGGGGGTGACAGATTAATTTGAGAACAGGAAACACTTGAAAT	601
Oy	566	TTTCAATTCACACGATTTGCAAGCTGAATGAGCCCAAGTGAAGTACGCGATTTG	621

Db 602 TTTCA TTTCA ACCAG TTTG CAAAG CTGA AATGA GCCC CAGTGA GGTCA GCGAT TAG 657

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RESULT 3
US-09-398-412B-1
/ Sequence 1, Application US/09398412B
/ Patent No. 6680380
/ GENERAL INFORMATION:
/ APPLICANT: Timans, Jacqueline C.
/ TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-12eta, related reagent
/ TITLE OF INVENTION: methods
/ FILE REFERENCE: DX0904K
/ CURRENT APPLICATION NUMBER: US/09/398,412B
/ CURRENT FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: US 60/100948
/ PRIOR FILING DATE: 1998-09-18
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1225
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (491)..(1144)
/ OTHER INFORMATION:
US-09-398-412B-1

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Query Match	78.5%	Score 510.4;	DB 4	Length 1225;
Best Local Similarity	97.9%;	Pred. No. 8.1e-150;		
Matches 517; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;

OY	99	TCCTTGCAGAGGTC	CCAAAGTGAAGAACTTAAACCCGAGAAATTCAGCATTCATGACCA	158
Db	625	TGTTTCACCAAGTGA	AGAGGTGAAGGCTTAAACCCGAGAAATTCAGCATTCATGACCA	684
OY	159	GGATTCACAAAGTACTG	TCTGTGAACCTGTGGAAATCTCATAGCAGTTCCAGATTAATACTA	218
Db	685	GGATTCACAAAGTACTG	GCTGTGAACCTGTGGAAATCTCATAGCAGTTCCAGATTAATACTA	744
OY	219	CATACGCCCAAGATCTT	TGATTAAGCTCATCCTTGAGCTCAGCCTCGCGAGAA	278
Db	745	CATACGCCCAAGATCTT	TGATTAAGCTCATCCTTGAGCTCAGCCTCGCGAGAA	804
OY	279	AGGAAGTCCAGTTCCT	CTCGGGGCTCTTAAAGGGAATTTGTCTTATCTGTGACAAAGA	338
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OY	339	TAAAGCAAAAGTCATCC	TTCAGCTGAAGAAAGGAAACGTGAAGAGCTGGCTGC	398
Db	865	TAAAGCAAAAGTCATCC	TTCAGCTGAAGAAAGGAAACGTGAAGAGCTGGCTGC	924
OY	399	CCAAAGGAATCAGACA	CGCGGCTTCATCTTTATAGGCTCAGGTGGGCTCCTGGAA	458
Db	925	CCAAAGGAATCAGACA	CGCGGCTTCATCTTTATAGGCTCAGGTGGGCTCCTGGAA	984
OY	459	CATGCTGAGTCCGGGCT	CACCCCGATGTTTCATCTGACCTTCCTGCAATTTGAATGA	518
Db	985	CATGCTGAGTCCGGGCT	CACCCCGATGTTTCATCTGACCTTCCTGCAATTTGAATGA	1044
OY	519	GCTGTGCGGGTGA	CAGATTAATTTGAGAAACAGGAACACATTTGAATTTTCATTCAAC	578
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OY	579	AGTTTGCAAGCTGAAT	GAGCCCGATGAGCTCAGCGATTTAGGGTAC	626
Db	1105	AGTTTGCAAGCTGAAT	GAGCCCGATGAGCTCAGCGATTTAGGGTAC	1152

RESULT 4  
 US-09-128-155-1  
 ; Sequence 1, Application US/09128155  
 ; Patent No. 6117654

```

; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (356)...(889)
US-09-128-155-1

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Query Match      61.1%; Score 397; DB 3; Length 989;
Best Local Similarity 97.6%; Pred. No. 36-114;
Matches 403; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 214 AACTACATACGCCGAGATCTTCTTGATAGGCTCCTGAGCTCAGCTCTGCG 273
    |||
DB 485 AATTGTGTCACAAAAGATCTTCTTGATAGGCTCCTGAGCTCAGCTCTGCG 544
    |||
QY 274 GAGAAAGGAAGTCCGATCTCTGAGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 333
    |||
DB 545 GAGAAAGGAAGTCCGATCTCTGAGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 604
    |||
QY 334 AAGGATAAGGACAAAGTCATCCTCTTCACTGAGGAGAGAACTGTAAGCTG 393
    |||
DB 605 AAGGATAAGGACAAAGTCATCCTCTTCACTGAGGAGAGAACTGTAAGCTG 664
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QY 394 GCTGCCCAAAAGGATCAGACGCGGCGCTTCATCTTTATAGGGCTCAGGTGAGCTCC 453
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DB 665 GCTGCCCAAAAGGATCAGACGCGGCGCTTCATCTTTATAGGGCTCAGGTGAGCTCC 724
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QY 454 TGAACATGCTGAGTCCGCGCTCACCCTGAGTGTTCATCTGACCTCTGCAATTGT 513
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DB 725 TGAACATGCTGAGTCCGCGCTCACCCTGAGTGTTCATCTGACCTCTGCAATTGT 784
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QY 514 AATGAGCTGTGGGTGACAGATTAATTGAGAACAGAAACACATTGAATTTTCATT 573
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DB 785 AATGAGCTGTGGGTGACAGATTAATTGAGAACAGAAACACATTGAATTTTCATT 844
    |||
QY 574 CAACGAGTTGCAAGCTGAATAGCCCCAGTGAAGTCAAGGATTAAGGTAC 626
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DB 845 CAACGAGTTGCAAGCTGAATAGCCCCAGTGAAGTCAAGGATTAAGGAAAC 897
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RESULT 5
US-09-128-155-10
; Sequence 10, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10

```

```

; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(408)
US-09-128-155-10

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Query Match      60.3%; Score 392.2; DB 3; Length 408;
Best Local Similarity 98.0%; Pred. No. 6.3e-113;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 214 AACTACATACGCCGAGATCTTCTTGATAGGCTCCTGAGCTCAGCTCTGCG 273
    |||
DB 4 AATTGTGTCACAAAAGATCTTCTTGATAGGCTCCTGAGCTCAGCTCTGCG 63
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QY 274 GAGAAAGGAAGTCCGATCTCTGAGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 333
    |||
DB 64 GAGAAAGGAAGTCCGATCTCTGAGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 123
    |||
QY 334 AAGGATAAGGACAAAGTCATCCTCTTCACTGAGGAGAGAACTGTAAGCTG 393
    |||
DB 124 AAGGATAAGGACAAAGTCATCCTCTTCACTGAGGAGAGAACTGTAAGCTG 183
    |||
QY 394 GCTGCCCAAAAGGATCAGACGCGGCGCTTCATCTTTATAGGGCTCAGGTGAGCTCC 453
    |||
DB 184 GCTGCCCAAAAGGATCAGACGCGGCGCTTCATCTTTATAGGGCTCAGGTGAGCTCC 243
    |||
QY 454 TGAACATGCTGAGTCCGCGCTCACCCTGAGTGTTCATCTGACCTCTGCAATTGT 513
    |||
DB 244 TGAACATGCTGAGTCCGCGCTCACCCTGAGTGTTCATCTGACCTCTGCAATTGT 303
    |||
QY 514 AATGAGCTGTGGGTGACAGATTAATTGAGAACAGAAACACATTGAATTTTCATT 573
    |||
DB 304 AATGAGCTGTGGGTGACAGATTAATTGAGAACAGAAACACATTGAATTTTCATT 363
    |||
QY 574 CAACGAGTTGCAAGCTGAATAGCCCCAGTGAAGTCAAGGATTAAGGTAC 618
    |||
DB 364 CAACGAGTTGCAAGCTGAATAGCCCCAGTGAAGTCAAGGATTAAGGTAC 408
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RESULT 6
US-09-128-155-6
; Sequence 6, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(501)
US-09-128-155-6

```

```

Query Match      60.3%; Score 392.2; DB 3; Length 501;
Best Local Similarity 98.0%; Pred. No. 6.9e-113;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 214 AACTACATACGCCGAGATCTTCTTGATAGGCTCCTGAGCTCAGCTCTGCG 273
    |||

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Db 97 AATTTGTTCAACAAGATCTTTCTTGATTAAGCTACTCTTGAGCTCAGCTCTGCG 156  
Qy 274 GAGAAAGAGAGTCCGATTTCTCCGCGGGGTCTCTAAAGGGAGTTTGTCTACTGTGAC 333  
Db 157 GAGAAAGAGAGTCCGATTTCTCCGCGGGGTCTCTAAAGGGAGTTTGTCTACTGTGAC 216  
Qy 334 AAGGATTAAGGACCAAGTATCATCTCTTCACTGAGAGAGAGAACTGATGAAGCTG 393  
Db 217 AAGGATTAAGGACCAAGTATCATCTCTTCACTGAGAGAGAACTGATGAAGCTG 276  
Qy 394 GCTGCCCAAAAGAAATCAGACGCGCGCTTCACTTTATAGGGCTCAGGTGGGGCTCC 453  
Db 277 GCTGCCCAAAAGAAATCAGACGCGCGCTTCACTTTATAGGGCTCAGGTGGGGCTCC 336  
Qy 454 TGGAAATGCTGAGTGGCGGCTCAACCCGAGTGGTTCATCTGACCTCTGCAATTGT 513  
Db 337 TGGAAATGCTGAGTGGCGGCTCAACCCGAGTGGTTCATCTGACCTCTGCAATTGT 396  
Qy 514 AATGAGCTGTTGGGGTGCAGATTAATTTGAGAACAGAAACACATTTGATTTTCAATT 573  
Db 397 AATGAGCTGTTGGGGTGCAGATTAATTTGAGAACAGAAACACATTTGATTTTCAATT 456  
Qy 574 CAACCAATTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCAT 618  
Db 457 CAACCAATTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCAT 501

RESULT 7  
US-09-128-155-3

; Sequence 3, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 534  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-128-155-3

Query Match 60.3%; Score 392.2; DB 3; Length 534;  
Best Local Similarity 98.0%; Pred. No. 7,1e-113;  
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 214 AACTACATACGCGCCAGAGATCTTTTGTGATTAGCTTACTTGAAGTCAAGCTCTGCG 273  
Db 130 AATTGTGTTCAACAAGATCTTTTGTGATTAGCTTACTTGAAGTCAAGCTCTGCG 189  
Qy 274 GAGAAAGAGTCCGATTTCTCTGCGGGGTCTTAAAGGGAGTTTGTCTACTGATAC 333  
Db 190 GAGAAAGAGTCCGATTTCTCTGCGGGGTCTTAAAGGGAGTTTGTCTACTGATAC 249  
Qy 334 AAGGATTAAGGACCAAGTATCATCTCTTCACTGAGAGAGAGAACTGATGAAGCTG 393  
Db 250 AAGGATTAAGGACCAAGTATCATCTCTTCACTGAGAGAGAGAACTGATGAAGCTG 309  
Qy 394 GCTGCCCAAAAGAAATCAGACGCGCGCTTCACTTTTATAGGGCTCAGGTGGGGCTCC 453  
Db 310 GCTGCCCAAAAGAAATCAGACGCGCGCTTCACTTTTATAGGGCTCAGGTGGGGCTCC 369  
Qy 454 TGGAAATGCTGAGTGGCGGCTCAACCCGAGTGGTTCATCTGACCTCTGCAATTGT 513  
Db 370 TGGAAATGCTGAGTGGCGGCTCAACCCGAGTGGTTCATCTGACCTCTGCAATTGT 429

Qy 514 AATGAGCTGTTGGGGTGCAGATTAATTTGAGAACAGAGAAACACATTTGATTTTCAATT 573  
Db 430 AATGAGCTGTTGGGGTGCAGATTAATTTGAGAACAGAGAAACACATTTGATTTTCAATT 489  
Qy 574 CAACCAATTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCAT 618  
Db 490 CAACCAATTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCAT 534

RESULT 8  
US-09-128-155-17

; Sequence 17, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 176373  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(176373)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-17

Query Match 38.9%; Score 252.8; DB 3; Length 176373;  
Best Local Similarity 99.2%; Pred. No. 7.5e-68;  
Matches 254; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 371 AGAAGAGAAACTGATGAAGTGGTGGCCCAAAAGAAATGACACGCGGGCTTCACTT 430  
Db 158957 AGAAGAGAAACTGATGAAGTGGTGGCCCAAAAGAAATGACACGCGGGCTTCACTT 159016  
Qy 431 TTATAGGGCTCAGGTGGGCTCTGGAACATGCTGAGTGGCGGCTCAACCCGGATGCT 490  
Db 159017 TTATAGGGCTCAGGTGGGCTCTGGAACATGCTGAGTGGCGGCTCAACCCGGATGCT 159076  
Qy 491 TCATCTGACCTCTGCAATTTGTAATGAGCTGTTGGGGTGCAGATTAATTTGAGAAC 550  
Db 159077 TCATCTGACCTCTGCAATTTGTAATGAGCTGTTGGGGTGCAGATTAATTTGAGAAC 159136  
Qy 551 GGAACAACATTTGATTTTCACTTCAACCAAGTTTGCAAGCTGAATGAGCCCGAGTGAAG 610  
Db 159137 GGAACAACATTTGATTTTCACTTCAACCAAGTTTGCAAGCTGAATGAGCCCGAGTGAAG 159196  
Qy 611 TCAGGATTAAGGGTAC 626  
Db 159197 TCAGGATTAAGGAAAC 159212

RESULT 9  
US-08-330-638D-1

; Sequence 1, Application US/08330638D  
; Patent No. 5731425  
; GENERAL INFORMATION:  
; APPLICANT: Brizzard, Billy  
; APPLICANT: Bianca, Darlene  
; APPLICANT: Chubet, Richard  
; APPLICANT: Wizard, Douglas  
; APPLICANT: Hopp, Thomas  
; TITLE OF INVENTION: POLYPEPTIDE SURFACE



;; TITLE OF INVENTION: MARKER FOR CELLS  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESSES: 10  
;; ADDRESSEE: Eastman Kodak Company,  
;; STREET: 343 State Street  
;; CITY: Rochester  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 14650-2201  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.5 inch,  
;; MEDIUM TYPE: 1.44 MB storage, (Hewlett Packard)  
;; COMPUTER: HP Vectra  
;; OPERATING SYSTEM: MS-DOS Version 6.0  
;; SOFTWARE: WORD FOR WINDOWS  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/330,638D  
;; FILING DATE: 28 OCT 1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA: NONE  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Kiernan, Anne B.  
;; REGISTRATION NUMBER: 36,566  
;; REFERENCE/DOCKET NUMBER: 71255  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (716) 588-2405  
;; TELEFAX: (716) 477-4646  
;;  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 204 base pairs  
;; TYPE: Nucleic Acid  
;; STRANDEDNESS: DOUBLE  
;; TOPOLOGY: Linear  
;; MOLECULE TYPE: SYNTHETIC GENE  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;;  
;; ORIGINAL SOURCE: SYNTHETICALLY PREPARED  
;; IMMEDIATE SOURCE: SYNTHETICALLY PREPARED  
;; FEATURE: SECRETION LEADER SEQUENCE  
;; FEATURE: LOCATION: 1-45  
;; FEATURE: FEATURE: CELL MARKER SEGMENT  
;; FEATURE: LOCATION: 46-69  
;; FEATURE: FEATURE: SPACER SEGMENT  
;; FEATURE: LOCATION: 70-132  
;; FEATURE: FEATURE: TRANSMEMBRANE SEGMENT  
;; FEATURE: LOCATION: 133-195  
;; FEATURE: FEATURE: ANCHOR SEGMENT  
;; FEATURE: LOCATION: 196-204  
;; PUBLICATION INFORMATION: NONE  
;;  
;; US-08-330-638D-1

Query Match 10.6%; Score 69; DB 1; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGTCTGACCTTCTGATCTTCTGTTGAGAGCTGAGCTGACTGACCTACCAAGCAGT 69  
DB 1 ATGTCTGACCTTCTGATCTTCTGTTGAGAGCTGAGCTGACTGACCTACCAAGCAGT 60

QY 70 GACGACAG 78  
DB 61 GACGACAG 69

RESULT 10  
US-08-906-746A-1  
; Sequence 1, Application US/08906746A  
; Patent No. 5945292  
; GENERAL INFORMATION:  
; APPLICANT: Brizzard, Billy L.  
; APPLICANT: Bianca, Darlene W.  
; APPLICANT: Chubert, Richard G.

;; APPLICANT: Vizard, Douglas L.  
;; APPLICANT: Hopp, Thomas P.  
;; TITLE OF INVENTION: Method of Identifying Cells with  
;; TITLE OF INVENTION: Polypeptide Surface Marker  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESSES: 10  
;; ADDRESSEE: Semigler, Powers, Leavitt & Roedel  
;; STREET: One Metropolitan Square- 16th Floor  
;; CITY: St. Louis  
;; STATE: Missouri  
;; COUNTRY: USA  
;; ZIP: 63102  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/906,746A  
;; FILING DATE: 06-AUG-1997  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stone, Paul A.  
;; REGISTRATION NUMBER: 38,628  
;; REFERENCE/DOCKET NUMBER: SGM 6874  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 314-231-5400  
;; TELEFAX: 314-231-4342  
;;  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 204 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;;  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: 1..45  
;; OTHER INFORMATION: /function= "Secretion leader  
;; OTHER INFORMATION: Sequence"  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: 46..69  
;; OTHER INFORMATION: /function= "Cell Marker Segment"  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: 70..132  
;; OTHER INFORMATION: /function= "Spacer Segment"  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: 133..195  
;; OTHER INFORMATION: /product= "Transmembrane Segment"  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: 196..204  
;; OTHER INFORMATION: /product= "Anchor Segment"  
;;  
;; US-08-906-746A-1

Query Match 10.6%; Score 69; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGTCTGACCTTCTGATCTTCTGTTGAGAGCTGAGCTGACTGACCTACCAAGCAGT 69  
DB 1 ATGTCTGACCTTCTGATCTTCTGTTGAGAGCTGAGCTGACTGACCTACCAAGCAGT 60

QY 70 GACGACAG 78  
DB 61 GACGACAG 69

RESULT 11  
US-08-644-271-31  
; Sequence 31, Application US/08644271  
; Patent No. 5814478  
; GENERAL INFORMATION:  
; APPLICANT: Valenzuela, et al.  
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS  
; TITLE OF INVENTION: AND LIGANDS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill Road  
; CITY: Tarrytown  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/644,271  
; FILING DATE: 10-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 60/008,657  
; FILING DATE: 15-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cobert, Robert J  
; REGISTRATION NUMBER: 36,108  
; REFERENCE/DOCKET NUMBER: REG 195A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 914-345-7400  
; TELEFAX: 914-345-7721  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1479 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1..1476  
; OTHER INFORMATION:  
; NAME/KEY: Human Agrin  
; LOCATION: 1..1479  
; OTHER INFORMATION:  
; US-08-644-271-31  
Query Match 10.6%; Score 69; DB 1; Length 1479;  
Best Local Similarity 100.0%; Pred. No. 3.8e-11;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 ATGTCTGACCTTCTAGCTCTTGTGGAGCTGAGCTGACTGACAAAGACGAT 69  
DB 1 ATGTCTGACCTTCTAGCTCTTGTGGAGCTGAGCTGACTGACAAAGACGAT 60  
QY 70 GACGACAAG 78  
DB 61 GACGACAAG 69  
RESULT 12  
US-09-077-955-35  
; Sequence 35, Application US/09077955A  
; Patent No. 6413740  
; GENERAL INFORMATION:  
; APPLICANT: Valenzuela et al., David M.  
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS  
; FILE REFERENCE: REG195-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/077,955A  
; CURRENT FILING DATE: 1998-09-10  
; EARLIER APPLICATION NUMBER: PCT/US96/20696  
; EARLIER FILING DATE: 1996-12-13  
; EARLIER APPLICATION NUMBER: 08/644,271  
; EARLIER FILING DATE: 1996-05-10  
; EARLIER APPLICATION NUMBER: 60/008,657  
; EARLIER FILING DATE: 1995-12-15  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 1479  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-077-955-35  
Query Match 10.6%; Score 69; DB 3; Length 1479;  
Best Local Similarity 100.0%; Pred. No. 3.8e-11;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 ATGTCTGACCTTCTAGCTCTTGTGGAGCTGAGCTGACTGACAAAGACGAT 69  
DB 1 ATGTCTGACCTTCTAGCTCTTGTGGAGCTGAGCTGACTGACAAAGACGAT 60  
QY 70 GACGACAAG 78  
DB 61 GACGACAAG 69  
RESULT 13  
US-07-977-451-7  
; Sequence 7, Application US/07977451  
; Patent No. 5270458  
; GENERAL INFORMATION:  
; APPLICANT: Lemischka, Ihor R.  
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Imclone Systems Incorporated  
; STREET: 180 Varick Street  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10014  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/977,451  
; FILING DATE: 19921119  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US UNASSIGNED  
; FILING DATE: 12-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/906,397  
; FILING DATE: 26-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/US92/05401  
; FILING DATE: 26-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: TW 81102961  
; FILING DATE: 15-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/US92/02750  
; FILING DATE: 02-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/813,593  
; FILING DATE: 24-DEC-1991  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/793,065  
FILING DATE: 15-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/728,913  
FILING DATE: 28-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/679,666  
FILING DATE: 02-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Felt, Irving N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: LEM-3-7P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-645-1405  
TELEFAX: 212-645-2054  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-977-451-7

Query Match 9.7%; Score 63.2; DB 1; Length 96;  
Best Local Similarity 89.5%; Pred. No. 6.5e-10;  
Matches 68; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TCACCATGTCGACCTTGATCTAGCTCTTGTGGAGCTGCACTGCTGACTACAAG 64  
DB 18 TCACCATGATGACCTTGATCTAGCTCTTGTGGAGCTGCTGCTGACTACAAG 77

QY 65 ACGATGACGACGACT 80  
DB 78 ATGATGATGACAAAGAT 93

## RESULT 14

US-08-252-517-7  
Sequence 7, Application US/08252517  
Patent No. 5548065  
GENERAL INFORMATION:  
APPLICANT: Lemischka, Ihor R.  
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Imclone Systems Incorporated  
STREET: 180 Varick Street  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10014  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/252,517  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,451  
FILING DATE: 19-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/906,397  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/05401  
FILING DATE: 26-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TM 81102961  
FILING DATE: 15-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/02750  
FILING DATE: 02-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,593  
FILING DATE: 24-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,065  
FILING DATE: 15-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/728,913  
FILING DATE: 28-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/679,666  
FILING DATE: 02-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Felt, Irving N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: LEM-3-7P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-645-1405  
TELEFAX: 212-645-2054  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-252-517-7

Query Match 9.7%; Score 63.2; DB 1; Length 96;  
Best Local Similarity 89.5%; Pred. No. 6.5e-10;  
Matches 68; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TCACCATGTCGACCTTGATCTAGCTCTTGTGGAGCTGCACTGCTGACTACAAG 64  
DB 18 TCACCATGATGACCTTGATCTAGCTCTTGTGGAGCTGCTGCTGACTACAAG 77

QY 65 ACGATGACGACGACT 80  
DB 78 ATGATGATGACAAAGAT 93

## RESULT 15

US-08-601-891-7  
Sequence 7, Application US/08601891  
Patent No. 5747651  
GENERAL INFORMATION:  
APPLICANT: Lemischka, Ihor R.  
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Imclone Systems Incorporated  
STREET: 180 Varick Street  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10014  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/601,891  
FILING DATE: 15-FEB-1996

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,451  
FILING DATE: 19-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/906,397  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/05401  
FILING DATE: 26-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: TW 81102961  
FILING DATE: 15-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US92/02750  
FILING DATE: 02-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,593  
FILING DATE: 24-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,065  
FILING DATE: 15-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/728,913  
FILING DATE: 28-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/679,666  
FILING DATE: 02-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Felt, Irving N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: LEM-3-7P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-645-1405  
TELEFAX: 212-645-2054  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-601-891-7

Query Match 9.7%; Score 63.2; DB 1; Length 96;  
Best Local Similarity 89.5%; Pred. No. 6.5e-10;  
Matches 68; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TCACCATGCTGCACCTTCTGATCCTTAGCTCTGTGGAGCTGCAGTTGCTGCTACTACAAG 64  
DB 18 TCACCATGAGTGACTCTGATCTTAGCCCTTGAGGAGCTGCTGTGCTGACTACAAG 77  
QY 65 ACGATGACGACAAGCT 80  
DB 78 ATGATGATGACAAGAT 93

Search completed: May 28, 2005, 17:23:11  
Job time : 163 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 28, 2005, 15:31:20 ; Search time 519 Seconds  
(without alignments)  
7689.236 Million cell updates/sec

Title: US-09-869-566-4

Perfect score: 650  
Sequence: 1 taatcaccatgctgcact.....cgactctagagatcccgag 650

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5700845 seqs, 306979757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
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8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09C\_NEW\_PUB.seq.\*  
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14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516.8	79.5	802	9	US-09-788-963-1
2	516.8	79.5	1600	15	US-10-302-554-1
3	516	79.4	579	18	US-09-876-790-1
4	516	79.4	579	18	US-10-888-918-1
5	516	79.4	579	19	US-10-888-779-1
6	516	79.4	579	19	US-10-888-867-1
7	516	79.4	579	19	US-10-888-780-1
8	516	79.4	579	19	US-10-888-931-1
9	515.2	79.3	657	17	US-10-695-195-3
10	515.2	79.3	657	17	US-10-694-978-3
11	515	79.2	657	10	US-09-876-790-5

12	515	79.2	657	18	US-10-888-918-5	Sequence 5, Appli
13	515	79.2	657	19	US-10-888-779-5	Sequence 5, Appli
14	515	79.2	657	19	US-10-888-867-5	Sequence 5, Appli
15	515	79.2	657	19	US-10-888-780-5	Sequence 5, Appli
16	515	79.2	657	19	US-10-888-931-5	Sequence 5, Appli
17	514	79.1	594	10	US-09-876-790-6	Sequence 6, Appli
18	514	79.1	594	18	US-10-888-918-6	Sequence 6, Appli
19	514	79.1	594	19	US-10-888-779-6	Sequence 6, Appli
20	514	79.1	594	19	US-10-888-867-6	Sequence 6, Appli
21	514	79.1	594	19	US-10-888-780-6	Sequence 6, Appli
22	514	79.1	594	19	US-10-888-931-6	Sequence 6, Appli
23	513.6	79.0	630	9	US-09-965-528-51	Sequence 51, Appli
24	513.6	79.0	630	11	US-09-969-984-51	Sequence 51, Appli
25	513	78.9	657	17	US-10-302-554-13	Sequence 13, Appli
26	510.4	78.5	1225	17	US-10-695-195-1	Sequence 1, Appli
27	510.4	78.5	1225	17	US-10-694-978-1	Sequence 1, Appli
28	505.8	77.8	754	13	US-10-06-867-141	Sequence 141, App
29	505.8	77.8	754	13	US-10-063-547-141	Sequence 141, App
30	505.8	77.8	754	13	US-10-063-551-141	Sequence 141, App
31	505.8	77.8	754	14	US-10-063-616-141	Sequence 141, App
32	505.8	77.8	754	14	US-10-063-569-141	Sequence 141, App
33	505.8	77.8	754	14	US-10-063-513-141	Sequence 141, App
34	505.8	77.8	754	14	US-10-063-515-141	Sequence 141, App
35	505.8	77.8	754	14	US-10-063-512-141	Sequence 141, App
36	505.8	77.8	754	14	US-10-063-502-141	Sequence 141, App
37	505.8	77.8	754	14	US-10-063-549-141	Sequence 141, App
38	505.8	77.8	754	14	US-10-063-554-141	Sequence 141, App
39	505.8	77.8	754	14	US-10-063-553-141	Sequence 141, App
40	505.8	77.8	754	14	US-10-063-518-141	Sequence 141, App
41	505.8	77.8	754	14	US-10-063-598-141	Sequence 141, App
42	505.8	77.8	754	14	US-10-227-693-141	Sequence 141, App
43	505.8	77.8	754	14	US-10-063-563-141	Sequence 141, App
44	505.8	77.8	754	14	US-10-063-555-141	Sequence 141, App
45	505.8	77.8	754	14	US-10-063-594-141	Sequence 141, App

ALIGNMENTS

RESULT 1  
US-09-788-963-1  
; Sequence 1, Application US/09788963  
; Patent No. US20020052473A1  
; GENERAL INFORMATION:  
; APPLICANT: YOUNG, PETER R.  
; APPLICANT: McDONNELL, PETER C.  
; APPLICANT: KUMAR, SANDAY  
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4  
; FILE REFERENCE: GP-70607-1C1  
; CURRENT APPLICATION NUMBER: US/09/788,963  
; PRIOR APPLICATION NUMBER: 09/293,625  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 09/452,140  
; PRIOR FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 802  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-788-963-1

Query Match 79.5%; Score 516.8; DB 9; Length 802;  
Best Local Similarity 98.7%; Pred. No. 5.1e-162;  
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 99 TCTTGCAGAGTCCCAAGGTAAGAACTTAACCCGAGAAATTCACATTCAGACCA 158  
DB 192 TGTTCACCAAGTCCCAAGGTAAGAACTTAACCCGAGAAATTCACATTCAGACCA 251  
QY 159 GGATCAACAAGTACTGTCTGCACTTCGGAATTCATACAGTTCCAGATTAATAACTA 218

Db 252 GGATCACAAGAGTCTGCTGCTGGAATCTCATAGCATTTCAATATAAACTA 311  
Qy 219 CATAGCCCAAGAGATCTTCTTGATAGCTCATCTTGAAGCTGCGGAGA 278  
Db 312 CATAGCCCAAGAGATCTTCTTGATAGCTCATCTTGAAGCTGCGGAGA 371  
Qy 279 AGAAGTCCGATCTCTGCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAGA 338  
Db 372 AGAAGTCCGATCTCTGCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAGA 431  
Qy 339 TAAAGACAAAGTCTCATCTTCAAGTGAAGAAAGAAATGATGAACTGCTGCG 398  
Db 432 TAAAGACAAAGTCTCATCTTCAAGTGAAGAAAGAAATGATGAACTGCTGCG 491  
Qy 399 CCAAGAGATCAGACAGCCCGGCTCTTCAATTTATAGGGCTCAGTGGCTCTGGA 458  
Db 432 CCAAGAGATCAGACAGCCCGGCTCTTCAATTTATAGGGCTCAGTGGCTCTGGA 551  
Qy 459 CATGCTGAGTGGCGGCTCACCCCGATGTTCACTTGCACCTCTGCAATTTGATGA 518  
Db 552 CATGCTGAGTGGCGGCTCACCCCGATGTTCACTTGCACCTCTGCAATTTGATGA 611  
Qy 519 GCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCACTTCAAC 578  
Db 612 GCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCACTTCAAC 671  
Qy 579 AGTTGCAAGCTGAATGAGCCCAAGTGAAGTCAAGCATTAAGGTAC 626  
Db 672 AGTTGCAAGCTGAATGAGCCCAAGTGAAGTCAAGCATTAAGGAAC 719

RESULT 2  
US-10-302-554-1  
; Sequence 1, Application US/10302554  
; Publication No. US20030148467A1  
; GENERAL INFORMATION:  
; APPLICANT: West, Robert R.  
; APPLICANT: Shepard, Paul O.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4  
; FILE REFERENCE: 98-59  
; CURRENT APPLICATION NUMBER: US/10/302,554  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US/09/428,118  
; PRIOR FILING DATE: 1999-10-27  
; PRIOR APPLICATION NUMBER: US 60/105,824  
; PRIOR FILING DATE: 1998-10-27  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1600  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (847) ... (1503)  
US-10-302-554-1

Query Match 79.5%; Score 516.8; DB 15; Length 1600;  
Best Local Similarity 98.7%; Pred. No. 7.3e-162;  
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 99 TCTTTGACAGAGTCCAAAGTGAAGAACTTAACCCGAAGAAATTCAGATTCATGACA 158  
Db 981 TCTTTACACAAATCCAAAGTGAAGAACTTAACCCGAAGAAATTCAGATTCATGACA 1040  
Qy 159 GGATCACAAGTACTGCTCTGGAATCTCATAGCAATTCAGATTAATACTA 218  
Db 1041 GGATCACAAGTACTGCTCTGGAATCTCATAGCAATTCAGATTAATACTA 1100  
Qy 219 CATAGCCCAAGAGATCTTCTTGATAGCTCATCTTGAAGCTGCGGAGA 278  
Db 1101 CATAGCCCAAGAGATCTTCTTGATAGCTCATCTTGAAGCTGCGGAGA 1160

Qy 279 AGAAGTCCGATCTCTGCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAGA 338  
Db 1161 AGAAGTCCGATCTCTGCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAGA 1220  
Qy 339 TAAAGACAAAGTCTCATCTTCAAGTGAAGAAAGAAATGATGAACTGCTGCG 398  
Db 1221 TAAAGACAAAGTCTCATCTTCAAGTGAAGAAAGAAATGATGAACTGCTGCG 1280  
Qy 399 CCAAGAGATCAGACAGCCCGGCTCTTCAATTTATAGGGCTCAGTGGCTCTGGA 458  
Db 1281 CCAAGAGATCAGACAGCCCGGCTCTTCAATTTATAGGGCTCAGTGGCTCTGGA 1340  
Qy 459 CATGCTGAGTGGCGGCTCACCCCGATGTTCACTTGCACCTCTGCAATTTGATGA 518  
Db 1341 CATGCTGAGTGGCGGCTCACCCCGATGTTCACTTGCACCTCTGCAATTTGATGA 1400  
Qy 519 GCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCACTTCAAC 578  
Db 1401 GCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCACTTCAAC 1460  
Qy 579 AGTTGCAAGCTGAATGAGCCCAAGTGAAGTCAAGCATTAAGGTAC 626  
Db 1461 AGTTGCAAGCTGAATGAGCCCAAGTGAAGTCAAGCATTAAGGAAC 1508

RESULT 3  
US-09-876-790-1  
; Sequence 1, Application US/09876790  
; Publication No. US20030091532A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECD DNAS AND POLYPEPTID  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/09/876,790  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-876-790-1

Query Match 79.4%; Score 516; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 7.9e-162;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 106 AGAGTCCAAAGTGAAGAACTTAACCCGAAGAAATTCAGATTCATGACAGGATAC 165  
Db 64 AGAGTCCAAAGTGAAGAACTTAACCCGAAGAAATTCAGATTCATGACAGGATAC 123  
Qy 166 AAAGTACTGCTCTGGAATCTCATAGCAATTCAGATTAATACTACATAGC 225  
Db 124 AAAGTACTGCTCTGGAATCTCATAGCAATTCAGATTAATACTACATAGC 183  
Qy 226 CCAAGATCTTCTTGATAGCTCATCTTGAAGCTCAGCTCTGCGAAGAAAGAGT 285  
Db 184 CCAAGATCTTCTTGATAGCTCATCTTGAAGCTCAGCTCTGCGAAGAAAGAGT 243  
Qy 286 CCGATTCCTGCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAGATTAAGA 345  
Db 244 CCGATTCCTGCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAGATTAAGA 303  
Qy 346 CAAAGTCAATCCCTTCAGCTGAAGAAAGAACTGATGAAGCTGCTGCCAAAG 405

Db 304 CAAAGCATCCATCCCTTCAAGTGAAGAAAGGAACTGATGAAGCTGCTGCCAAAAG 363  
Qy 406 GAATGACAGCGCGCGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 465  
Db 364 GAATGACAGCGCGCGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 423  
Qy 466 GAGTGGCGGCTCACCCCGGATGCTCATCTGCACTCTGCAATTGTATAGGCTGTT 525  
Db 424 GAGTGGCGGCTCACCCCGGATGCTCATCTGCACTCTGCAATTGTATAGGCTGTT 483  
Qy 526 GGGGTGACAGATTAATTGAGAAACAGAAACATTTGAAATTTTCAACCAAGTTTC 585  
Db 484 GGGGTGACAGATTAATTGAGAAACAGAAACATTTGAAATTTTCAACCAAGTTTC 543  
Qy 586 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCATTAG 621  
Db 544 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCATTAG 579

## RESULT 4

US-10-888-918-1  
; Sequence 1, Application US/10888918  
; Publication No. US20040248187A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND XRE2 DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,918  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-918-1

Query Match 79.4%; Score 516; DB 18; Length 579;  
Best Local Similarity 100.0%; Pred. No. 7.9e-162;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 AGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 165  
Db 64 AGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 123  
Qy 166 AAAGTACTGCTCTGAGCTCTGGAATCTCATAGCACTTCCAGATTAATACTACATAGCC 225  
Db 124 AAAGTACTGCTCTGAGCTCTGGAATCTCATAGCACTTCCAGATTAATACTACATAGCC 183  
Qy 226 CCAGAGATCTTCTTTCATTTAGCTCATCTTGAAGTCAAGCTCCGGAAGAAAGAAAT 285  
Db 184 CCAGAGATCTTCTTTCATTTAGCTCATCTTGAAGTCAAGCTCCGGAAGAAAGAAAT 243  
Qy 286 CCAGATCTCTGAGGCTCTCTAAAGGGAATTTGTCTCTACTGTGACAAAGATTAAGGA 345  
Db 244 CCAGATCTCTGAGGCTCTCTAAAGGGAATTTGTCTCTACTGTGACAAAGATTAAGGA 303  
Qy 346 CAAAGTCAATCCCTTCACTGTAAGAAAGAACTGATGAAGTGGCTGCCAAAAG 405  
Db 304 CAAAGTCAATCCCTTCACTGTAAGAAAGAACTGATGAAGTGGCTGCCAAAAG 363  
Qy 406 GAATGACAGCGCGCGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 465

Db 364 GAATGACAGCGCGCGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 423  
Qy 466 GAGTGGCGGCTCACCCCGGATGCTCATCTGCACTCTGCAATTGTATAGGCTGTT 525  
Db 424 GAGTGGCGGCTCACCCCGGATGCTCATCTGCACTCTGCAATTGTATAGGCTGTT 483  
Qy 526 GGGGTGACAGATTAATTGAGAAACAGAAACATTTGAAATTTTCAACCAAGTTTC 585  
Db 484 GGGGTGACAGATTAATTGAGAAACAGAAACATTTGAAATTTTCAACCAAGTTTC 543  
Qy 586 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCATTAG 621  
Db 544 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCATTAG 579

## RESULT 5

US-10-888-779-1  
; Sequence 1, Application US/10888779  
; Publication No. US2005009138A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND XRE2 DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,779  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-779-1

Query Match 79.4%; Score 516; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 7.9e-162;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 AGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 165  
Db 64 AGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 123  
Qy 166 AAAGTACTGCTCTGAGCTCTGGAATCTCATAGCACTTCCAGATTAATACTACATAGCC 225  
Db 124 AAAGTACTGCTCTGAGCTCTGGAATCTCATAGCACTTCCAGATTAATACTACATAGCC 183  
Qy 226 CCAGAGATCTTCTTTCATTTAGCTCATCTTGAAGTCAAGCTCCGGAAGAAAGAAAT 285  
Db 184 CCAGAGATCTTCTTTCATTTAGCTCATCTTGAAGTCAAGCTCCGGAAGAAAGAAAT 243  
Qy 286 CCAGATCTCTGAGGCTCTCTAAAGGGAATTTGTCTCTACTGTGACAAAGATTAAGGA 345  
Db 244 CCAGATCTCTGAGGCTCTCTAAAGGGAATTTGTCTCTACTGTGACAAAGATTAAGGA 303  
Qy 346 CAAAGTCAATCCCTTCACTGTAAGAAAGAACTGATGAAGTGGCTGCCAAAAG 405  
Db 304 CAAAGTCAATCCCTTCACTGTAAGAAAGAACTGATGAAGTGGCTGCCAAAAG 363  
Qy 406 GAATGACAGCGCGCGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 465  
Db 364 GAATGACAGCGCGCGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 423  
Qy 466 GAGTGGCGGCTCACCCCGGATGCTCATCTGCACTCTGCAATTGTATAGGCTGTT 525

Db 424 GAGTGGCGGCTCACCCCGAGTGTCACTGACCTCTGCAATTGATATAGAGCTGTT 483  
QY 526 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTGTC 585  
Db 484 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTGTC 543  
QY 586 AAAGCTGAATATAGCCCCAGTGTGAGTCAAGCATTTAG 621  
Db 544 AAAGCTGAATATAGCCCCAGTGTGAGTCAAGCATTTAG 579

RESULT 6  
US-10-888-867-1  
; Sequence 1, Application US/10888867  
; Publication No. US2005009075A1  
; GENERAL INFORMATION:  
; APPLICANT: STMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND XRE2 DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,867  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-867-1

Query Match 79.4%; Score 516; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 7.9e-162; Indels 0; Gaps 0;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 AGAGTCCAAAGTGAAGAACTTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 165  
Db 64 AAGGTCCAAAGTGAAGAACTTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 123  
QY 166 AAAGTACTGTCTGTGACTCTGGAATCTCATGACAGTTCCAGATTAATACTACATACGC 225  
Db 124 AAAGTACTGTCTGTGACTCTGGAATCTCATGACAGTTCCAGATTAATACTACATACGC 183  
QY 226 CCAGAGATCTTCTTTCATTAAGCTTCATGAGCTGAGCTGCGGAGAAAGAAAT 285  
Db 184 CCAGAGATCTTCTTTCATTAAGCTTCATGAGCTGAGCTGCGGAGAAAGAAAT 243  
QY 286 CCGATTCTCTGGGGGTCTCTAAAGGGAGATTGCTCTACTGTGACAAGATTAAGGA 345  
Db 244 CCGATTCTCTGGGGGTCTCTAAAGGGAGATTGCTCTACTGTGACAAGATTAAGGA 303  
QY 346 CAAAGTCAATCCCTTCAGTGAAGAAAGAACTGATGAAGCTGCTGCCAAAAG 405  
Db 304 CAAAGTCAATCCCTTCAGTGAAGAAAGAACTGATGAAGCTGCTGCCAAAAG 363  
QY 406 GAATCAGACGCGCGGCTTCATCTTTATAGGGCTCAGTGGGCTCTGGAACATGCTG 465  
Db 364 GAATCAGACGCGCGGCTTCATCTTTATAGGGCTCAGTGGGCTCTGGAACATGCTG 423  
QY 466 GAGTGGGGGCTCACCCCGAGATGTTTCATCTGCACTCTGCAATTTGTAATGAGCTGTT 525  
Db 424 GAGTGGGGGCTCACCCCGAGATGTTTCATCTGCACTCTGCAATTTGTAATGAGCTGTT 483  
QY 526 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTGTC 585

Db 484 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTGTC 543  
QY 586 AAAGCTGAATATAGCCCCAGTGTGAGTCAAGCATTTAG 621  
Db 544 AAAGCTGAATATAGCCCCAGTGTGAGTCAAGCATTTAG 579

RESULT 7  
US-10-888-780-1  
; Sequence 1, Application US/10888780  
; Publication No. US20050013797A1  
; GENERAL INFORMATION:  
; APPLICANT: STMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND XRE2 DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,780  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-780-1

Query Match 79.4%; Score 516; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 7.9e-162; Indels 0; Gaps 0;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 AGAGTCCAAAGTGAAGAACTTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 165  
Db 64 AAGGTCCAAAGTGAAGAACTTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 123  
QY 166 AAAGTACTGTCTGTGACTCTGGAATCTCATGACAGTTCCAGATTAATACTACATACGC 225  
Db 124 AAAGTACTGTCTGTGACTCTGGAATCTCATGACAGTTCCAGATTAATACTACATACGC 183  
QY 226 CCAGAGATCTTCTTTCATTAAGCTTCATGAGCTGAGCTGCGGAGAAAGAAAT 285  
Db 184 CCAGAGATCTTCTTTCATTAAGCTTCATGAGCTGAGCTGCGGAGAAAGAAAT 243  
QY 286 CCGATTCTCTGGGGGTCTCTAAAGGGAGATTGCTCTACTGTGACAAGATTAAGGA 345  
Db 244 CCGATTCTCTGGGGGTCTCTAAAGGGAGATTGCTCTACTGTGACAAGATTAAGGA 303  
QY 346 CAAAGTCAATCCCTTCAGTGAAGAAAGAACTGATGAAGCTGCTGCCAAAAG 405  
Db 304 CAAAGTCAATCCCTTCAGTGAAGAAAGAACTGATGAAGCTGCTGCCAAAAG 363  
QY 406 GAATCAGACGCGCGGCTTCATCTTTATAGGGCTCAGTGGGCTCTGGAACATGCTG 465  
Db 364 GAATCAGACGCGCGGCTTCATCTTTATAGGGCTCAGTGGGCTCTGGAACATGCTG 423  
QY 466 GAGTGGGGGCTCACCCCGAGATGTTTCATCTGCACTCTGCAATTTGTAATGAGCTGTT 525  
Db 424 GAGTGGGGGCTCACCCCGAGATGTTTCATCTGCACTCTGCAATTTGTAATGAGCTGTT 483  
QY 526 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTGTC 585  
Db 484 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTGTC 543  
QY 586 AAAGCTGAATATAGCCCCAGTGTGAGTCAAGCATTTAG 621



Db 544 AAAGCTGAATGATGCCCCAGTAGGTCAGGATTAAG 579

RESULT 8  
US-10-888-931-1

; Sequence 1, Application US/10888931  
; Publication No. US20050013798A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECC DNAs AND POLYPEPT  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,931  
; CURRENT FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 1  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-931-1

Query Match 79.4%; Score 516; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 7.9e-162;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

106 AGAGGTCCAAGGTGAAGACTTAAACCCGAGAATTCAGATTCATGACCGAGATCAC 165  
64 AGAGGTCCAAGGTGAAGACTTAAACCCGAGAATTCAGATTCATGACCGAGATCAC 123  
166 AAAGTACTGCTCTGAGCTCTGGAATCTCATAGAGTTCCAGATTAATACTACATACGC 225  
124 AAAGTACTGCTCTGAGCTCTGGAATCTCATAGAGTTCCAGATTAATACTACATACGC 183  
226 CCAGAGATTTCTTTGCAATTAAGCTTCATCTTGAAGCTCTGCGAGAAAGAAAGT 285  
184 CCAGAGATTTCTTTGCAATTAAGCTTCATCTTGAAGCTCTGCGAGAAAGAAAGT 243  
286 CCAGATTCCTGCGAGGTCTCTAAAGGGAGTTTGTCTTACTGTGACAAGATTAAGA 345  
244 CCAGATTCCTGCGAGGTCTCTAAAGGGAGTTTGTCTTACTGTGACAAGATTAAGA 303  
346 CAAAGTCATCATCCCTTCAGCTGAAGAAAGAACTGATGAAGCTGCTGCCAAAG 405  
304 CAAAGTCATCATCCCTTCAGCTGAAGAAAGAACTGATGAAGCTGCTGCCAAAG 363  
406 GAATCAGACGCGCGGCTTCATCTTTAAGGGCTCAGGTGGGCTCTCGAAACATGCTG 465  
364 GAATCAGACGCGCGGCTTCATCTTTAAGGGCTCAGGTGGGCTCTCGAAACATGCTG 423  
466 GAGTGGGCGGCTCACCCGGATGCTTCATCTGCACTCTGCAATTTGATAGAGCTGTT 525  
424 GAGTGGGCGGCTCACCCGGATGCTTCATCTGCACTCTGCAATTTGATAGAGCTGTT 483  
526 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCAATTCACAGTTTC 585  
484 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCAATTCACAGTTTC 543  
586 AAAGCTGAATGATGCCCCAGTAGGTCAGGATTAAG 621  
544 AAAGCTGAATGATGCCCCAGTAGGTCAGGATTAAG 579

RESULT 9  
US-10-695-195-3

; Sequence 3, Application US/10695195  
; Publication No. US20040068099A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/695,195

FILING DATE: 27-Oct-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/398,412

FILING DATE: 17-Sep-1999

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0904K

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)852-9196

TELEFAX: (650)496-1200

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 657 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..654

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-695-195-3

Query Match 79.3%; Score 515.2; DB 17; Length 657;  
Best Local Similarity 97.6%; Pred. No. 1.6e-161;

Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

86 CCGGAATTCAGCTCTTTCAGAGGTCCAAAGGTGAAGACTTAAACCCGAGAATTCGA 145  
122 CCGCATGAATTTTGTTCACAAAGTCCAAAGGTGAAGACTTAAACCCGAGAATTCGA 181  
146 GCAATTCATGACAGATTCACAAAGTACTGCTCTGAGCTCTGGAATCTCATAGCAGTTT 205  
182 GCAATTCATGACAGATTCACAAAGTACTGCTCTGAGCTCTGGAATCTCATAGCAGTTT 241  
206 CAGATTAATACTACATGAGCCGAGAGATCTCTTTGCAATTAAGCTTCATCTTGAAGCTG 265  
242 CAGATTAATACTACATGAGCCGAGAGATCTCTTTGCAATTAAGCTTCATCTTGAAGCTG 301  
266 CCTTGGCGAGAAAGAGTCCGATTTCTCTGAGGAGTCTTAAAGGGAGTTTGTCTCT 325  
302 CCTTGGCGAGAAAGAGTCCGATTTCTCTGAGGAGTCTTAAAGGGAGTTTGTCTCT 361  
326 ACTGTGACAAAGATTAAGGACAAAGTCAATCCCTTCAGCTGAGTGAAGAGAAACTGA 385  
362 ACTGTGACAAAGATTAAGGACAAAGTCAATCCCTTCAGCTGAGTGAAGAGAAACTGA 421  
386 TGAAGCTGGCTGCCAAAGAAAGATCAGACGCGGCGCTTCATCTTTAATAGGCTCAGG 445

Db 422 TGAAGCTGGCTGCCCAAAAAGAAATAGACACGCCGCCCTTCACTTTATATAGGCTCAGG 481  
Qy 446 TGGGCTCCCTGAACAATGCTGAGTGGCGCGCTCACCCCGAATGTTCACTGACCTCCT 505  
Db 482 TGGGCTCCCTGAACAATGCTGAGTGGCGCGCTCACCCCGAATGTTCACTGACCTCCT 541  
Qy 506 GCAATTGATATAGAGCTGTTGGGGGTGACAGATTAATTGAGAAACAGAAACATTGAAT 565  
Db 542 GCAATTGATATAGAGCTGTTGGGGGTGACAGATTAATTGAGAAACAGAAACATTGAAT 601  
Qy 566 TTTCAATTCAACCAAGTTTGCAAGCTGAAATAGAGCCCGAGTGGCTCAGCGATTAG 621  
Db 602 TTTCAATTCAACCAAGTTTGCAAGCTGAAATAGAGCCCGAGTGGCTCAGCGATTAG 657

RESULT 10  
US-10-694-978-3

Sequence 3, Application US/10694978  
Publication No. US20040087766A1  
GENERAL INFORMATION:  
APPLICANT: Timans, Jacqueline C.  
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/10/694,978  
APPLICATION NUMBER: US/10/694,978  
FILING DATE: 27-Oct-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/398,412  
FILING DATE: 17-Sep-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0904K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-9196  
TELEFAX: (650) 496-1200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 657 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..654  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-694-978-3

Query Match 79.3%; Score 515.2; DB 17; Length 657;  
Best Local Similarity 97.6%; Pred. No. 1.6e-161;  
Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 86 CCGCGAATTCAGCTCTTGGCAGAGGTCCAAGGTGAAGACTTAAACCGAAGAAATTCA 145  
Db 122 CCGCGAATTCAGCTCTTGGCAGAGGTCCAAGGTGAAGACTTAAACCGAAGAAATTCA 181  
Qy 146 GCAATTCATGACCAAGATCAAAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCAGTTG 205  
Db 182 GCAATTCATGACCAAGATCAAAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCAGTTG 241

Qy 206 CAGATAAAACCTACATACGAGATCTTCTTGTGACATTAAGCTTCATCTTGAAGCTGAG 265  
Db 242 CAGATAAAACCTACATACGAGATCTTCTTGTGACATTAAGCTTCATCTTGAAGCTGAG 301  
Qy 266 CCTCTGCGGAGAAAGAGATCCGATTTCTCTGGGGGGTCTTAAAGGGAGTTTGTCT 325  
Db 302 CCTCTGCGGAGAAAGAGATCCGATTTCTCTGGGGGGTCTTAAAGGGAGTTTGTCT 361  
Qy 326 ACTGTGACAAAGATTAAGGACAAAGTCAATCCCTTCAGCTGAGAAAGAGAAATGCA 385  
Db 362 ACTGTGACAAAGATTAAGGACAAAGTCAATCCCTTCAGCTGAGAAAGAGAAATGCA 421  
Qy 386 TGAAGCTGGCTGCCCAAAAAGAAATAGACACGCCGCCCTTCACTTTATATAGGCTCAGG 445  
Db 422 TGAAGCTGGCTGCCCAAAAAGAAATAGACACGCCGCCCTTCACTTTATATAGGCTCAGG 481  
Qy 446 TGGGCTCCCTGAACAATGCTGAGTGGCGCGCTCACCCCGAATGTTCACTGACCTCCT 505  
Db 482 TGGGCTCCCTGAACAATGCTGAGTGGCGCGCTCACCCCGAATGTTCACTGACCTCCT 541  
Qy 506 GCAATTGATATAGAGCTGTTGGGGGTGACAGATTAATTGAGAAACAGAAACATTGAAT 565  
Db 542 GCAATTGATATAGAGCTGTTGGGGGTGACAGATTAATTGAGAAACAGAAACATTGAAT 601  
Qy 566 TTTCAATTCAACCAAGTTTGCAAGCTGAAATAGAGCCCGAGTGGCTCAGCGATTAG 621  
Db 602 TTTCAATTCAACCAAGTTTGCAAGCTGAAATAGAGCCCGAGTGGCTCAGCGATTAG 657

RESULT 11  
US-09-876-790-5

Sequence 5, Application US/09876790  
Publication No. US20030091532A1  
GENERAL INFORMATION:  
APPLICANT: SIMS, John E.  
APPLICANT: SMITH, Dirk E.  
APPLICANT: BORN, Teresa L.  
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTIDES  
FILE REFERENCE: 2008-US  
CURRENT APPLICATION NUMBER: US/09/876,790  
FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 60/112,163  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: 60/146,675  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: PCT/US99/29549  
PRIOR FILING DATE: 1999-12-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 657  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-876-790-5

Query Match 79.2%; Score 515; DB 10; Length 657;  
Best Local Similarity 99.0%; Pred. No. 1.8e-161;  
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 99 TCTTTCAGAGGTCCAAAGGTGAAGACTTAAACCGAAGAAATTCAGATTCATGACCA 158  
Db 135 TCTTTCAGAGGTCCAAAGGTGAAGACTTAAACCGAAGAAATTCAGATTCATGACCA 194  
Qy 159 GGATCACAAAGTACGTGCTGAGCTCTGGGAATCTCATAGAGTTCAGATTAATACTA 218  
Db 195 GGATCACAAAGTACGTGCTGAGCTCTGGGAATCTCATAGAGTTCAGATTAATACTA 254  
Qy 219 CATAGCCCAAGATCTTCTTGTGACATTAAGCTTCATCTTGAAGCTCAGCTCTGCGAGAA 278  
Db 255 CATAGCCCAAGATCTTCTTGTGACATTAAGCTTCATCTTGAAGCTCAGCTCTGCGAGAA 314  
Qy 279 AGAAGTCGATTCCTCTGGGGGTCTTAAAGGGAAGTTTGTCTCTACTGACAAAGA 338

DB 315 AGAAGATCCGATTCCTCTGGGGGTCTCTAAGGGAGGTTTGTCTACTGTGACAAGGA 374  
QY 339 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGGAAGAACTGATGAAGCTGCTGC 398  
DB 375 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGGAAGAACTGATGAAGCTGCTGC 434  
QY 399 CCAAAAGGATGACGACGCGCGCTTCACTTTTATAGGGCTCAGTGGGCTCTCGAA 458  
DB 435 CCAAAAGGATGACGACGCGCGCTTCACTTTTATAGGGCTCAGTGGGCTCTCGAA 494  
QY 459 CATGCTGAGTGGGGGCTCACCCTGGAGTTCATCTGCACTCTGCAATTGTATGA 518  
DB 495 CATGCTGAGTGGGGGCTCACCCTGGAGTTCATCTGCACTCTGCAATTGTATGA 554  
QY 519 GCCTGTTGGGGGTGACAGATAAATTGAGAACAGAAACATTTGATTTTCAATTTCAACC 578  
DB 555 GCCTGTTGGGGGTGACAGATAAATTGAGAACAGAAACATTTGATTTTCAATTTCAACC 614  
QY 579 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 621  
DB 615 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 657

## RESULT 12

US-10-888-918-5  
; Sequence 5, Application US/10888918  
; Publication No. US20040248187A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,918  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 657  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-918-5

Query Match 79.2%; Score 515; DB 18; Length 657;  
Best Local Similarity 99.0%; Pred. No. 1.8e-161;  
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 99 TCTTTGACAGAGTCCAAAGTGAAGAACTTAAACCCGAAAGAAATTGACATTCATGACCA 158  
DB 135 TGTTCACACAAAGTCCAAAGTGAAGAACTTAAACCCGAAAGAAATTGACATTCATGACCA 194  
QY 159 GGATCACAAAGTACGTCTGTGAGCTCTGGGAATCTCATAGCAGTCCAGATTTAAACTA 218  
DB 195 GGATCACAAAGTACGTCTGTGAGCTCTGGGAATCTCATAGCAGTCCAGATTTAAACTA 254  
QY 219 CATAGCCCAAGAGATCTTCTTGACATTTAGCCTCATCTGAGCTCAGCTCTGCGAGAA 278  
DB 255 CATAGCCCAAGAGATCTTCTTGACATTTAGCCTCATCTGAGCTCAGCTCTGCGAGAA 314  
QY 279 AGGAAGTCCGATTCCTCTGGGGGTCTCTAAAGGGAGTTTGTCTTACTGTGACAAGGA 338  
DB 315 AGGAAGTCCGATTCCTCTGGGGGTCTCTAAAGGGAGTTTGTCTTACTGTGACAAGGA 374  
QY 339 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGGAAGAACTGATGAAGCTGCTGC 398

DB 375 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGGAAGAACTGATGAAGCTGCTGC 434  
QY 399 CCAAAAGGATGACGACGCGCGCTTCACTTTTATAGGGCTCAGTGGGCTCTCGAA 458  
DB 435 CCAAAAGGATGACGACGCGCGCTTCACTTTTATAGGGCTCAGTGGGCTCTCGAA 494  
QY 459 CATGCTGAGTGGGGGCTCACCCTGGAGTTCATCTGCACTCTGCAATTGTATGA 518  
DB 495 CATGCTGAGTGGGGGCTCACCCTGGAGTTCATCTGCACTCTGCAATTGTATGA 554  
QY 519 GCCTGTTGGGGGTGACAGATAAATTGAGAACAGAAACATTTGATTTTCAATTTCAACC 578  
DB 555 GCCTGTTGGGGGTGACAGATAAATTGAGAACAGAAACATTTGATTTTCAATTTCAACC 614  
QY 579 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 621  
DB 615 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 657

## RESULT 13

US-10-888-779-5  
; Sequence 5, Application US/10888779  
; Publication No. US20050009138A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,779  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 657  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-779-5

Query Match 79.2%; Score 515; DB 19; Length 657;  
Best Local Similarity 99.0%; Pred. No. 1.8e-161;  
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 99 TCTTTGACAGAGTCCAAAGTGAAGAACTTAAACCCGAAAGAAATTGACATTCATGACCA 158  
DB 135 TGTTCACACAAAGTCCAAAGTGAAGAACTTAAACCCGAAAGAAATTGACATTCATGACCA 194  
QY 159 GGATCACAAAGTACGTCTGTGAGCTCTGGGAATCTCATAGCAGTCCAGATTTAAACTA 218  
DB 195 GGATCACAAAGTACGTCTGTGAGCTCTGGGAATCTCATAGCAGTCCAGATTTAAACTA 254  
QY 219 CATAGCCCAAGAGATCTTCTTGACATTTAGCCTCATCTGAGCTCAGCTCTGCGAGAA 278  
DB 255 CATAGCCCAAGAGATCTTCTTGACATTTAGCCTCATCTGAGCTCAGCTCTGCGAGAA 314  
QY 279 AGGAAGTCCGATTCCTCTGGGGGTCTCTAAAGGGAGTTTGTCTTACTGTGACAAGGA 338  
DB 315 AGGAAGTCCGATTCCTCTGGGGGTCTCTAAAGGGAGTTTGTCTTACTGTGACAAGGA 374  
QY 339 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGGAAGAACTGATGAAGCTGCTGC 398  
DB 375 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGGAAGAACTGATGAAGCTGCTGC 434  
QY 399 CCAAAAGGATGACGACGCGCGCTTCACTTTTATAGGGCTCAGTGGGCTCTCGAA 458

DB 435 CCAAAAGGATCGAGCGCGGCTTCATCTTTTATAGGGCTCAGGTGGCTCCGGAA 494  
QY 459 CATGCTGAGTGGGGGCTCAACCCGGAGTTCATCTGACCTCTGCAATTTGTAATA 518  
DB 495 CATGCTGAGTGGGGGCTCAACCCGGAGTTCATCTGACCTCTGCAATTTGTAATA 554  
QY 519 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAACC 578  
DB 555 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAACC 614  
QY 579 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAGTCAAGCATTTAG 621  
DB 615 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAGTCAAGCATTTAG 657

## RESULT 14

US-10-888-867-5  
; Sequence 5, Application US/1088867  
; Publication No. US2005009075A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECC DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,867  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 657  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-867-5

Query Match 79.2%; Score 515; DB 19; Length 657;  
Best Local Similarity 99.0%; Pred. No. 1.8e-161;  
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 99 TCTTTGACAGAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCA 158  
DB 135 TCTTACACAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCA 194  
QY 159 GGATCACAAAGTACTGCTCTGGAATCTGGAATCTGATGAGTCCGATTAATACTA 218  
DB 195 GGATCACAAAGTACTGCTCTGGAATCTGGAATCTGATGAGTCCGATTAATACTA 254  
QY 219 CATAGCCCAAGATCTTCTTGGATTAGCTTCATCTGAGCTGAGCTCTGCGAGAA 278  
DB 255 CATAGCCCAAGATCTTCTTGGATTAGCTTCATCTGAGCTGAGCTCTGCGAGAA 314  
QY 279 AGGAAGTCCGATTCCTGCGGGGTCTTAAGGGAGTTTGTCTCTACTGTGACAGAA 338  
DB 315 AGGAAGTCCGATTCCTGCGGGGTCTTAAGGGAGTTTGTCTCTACTGTGACAGAA 374  
QY 339 TAAAGACAAAGTCAATCCCTTCACTGAGTGAAGAGAGAACTGATGAGTGGCTGC 398  
DB 375 TAAAGACAAAGTCAATCCCTTCACTGAGTGAAGAGAGAACTGATGAGTGGCTGC 434  
QY 399 CCAAAAGGATGACAGCGCGGCTTCATCTTTTATAGGGCTCAGGTGGCTCCGAGAA 458  
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QY 459 CATGCTGAGTGGGGGCTCAACCCGGAGTTCATCTGACCTCTGCAATTTGTAATA 518

DB 495 CATGCTGAGTGGGGGCTCAACCCGGAGTTCATCTGACCTCTGCAATTTGTAATA 554  
QY 519 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAACC 578  
DB 555 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAACC 614  
QY 579 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAGTCAAGCATTTAG 621  
DB 615 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAGTCAAGCATTTAG 657

## RESULT 15

US-10-888-780-5  
; Sequence 5, Application US/10888780  
; Publication No. US20050013797A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECC DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,780  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 657  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-780-5

Query Match 79.2%; Score 515; DB 19; Length 657;  
Best Local Similarity 99.0%; Pred. No. 1.8e-161;  
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 99 TCTTTGACAGAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCA 158  
DB 135 TCTTACACAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCA 194  
QY 159 GGATCACAAAGTACTGCTCTGGAATCTGGAATCTGATGAGTCCGATTAATACTA 218  
DB 195 GGATCACAAAGTACTGCTCTGGAATCTGGAATCTGATGAGTCCGATTAATACTA 254  
QY 219 CATAGCCCAAGATCTTCTTGGATTAGCTTCATCTGAGCTGAGCTCTGCGAGAA 278  
DB 255 CATAGCCCAAGATCTTCTTGGATTAGCTTCATCTGAGCTGAGCTCTGCGAGAA 314  
QY 279 AGGAAGTCCGATTCCTGCGGGGTCTTAAGGGAGTTTGTCTCTACTGTGACAGAA 338  
DB 315 AGGAAGTCCGATTCCTGCGGGGTCTTAAGGGAGTTTGTCTCTACTGTGACAGAA 374  
QY 339 TAAAGACAAAGTCAATCCCTTCACTGAGTGAAGAGAGAACTGATGAGTGGCTGC 398  
DB 375 TAAAGACAAAGTCAATCCCTTCACTGAGTGAAGAGAGAACTGATGAGTGGCTGC 434  
QY 399 CCAAAAGGATGACAGCGCGGCTTCATCTTTTATAGGGCTCAGGTGGCTCCGAGAA 458  
DB 435 CCAAAAGGATGACAGCGCGGCTTCATCTTTTATAGGGCTCAGGTGGCTCCGAGAA 494  
QY 459 CATGCTGAGTGGGGGCTCAACCCGGAGTTCATCTGACCTCTGCAATTTGTAATA 518  
DB 495 CATGCTGAGTGGGGGCTCAACCCGGAGTTCATCTGACCTCTGCAATTTGTAATA 554  
QY 519 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAACC 578

Db 555 |||||  
GCCTGTTGGGGTGACAGATTAATTGGAGAACAGGAAACACATTGAATTTTCATTTCACACC 614

Qy 579 AGTTTGCAAAAGCTGAATGAGCCCCCAGTGAGGTCAAGGATTAG 621  
615 AGTTTGCAAAAGCTGAATGAGCCCCCAGTGAGGTCAAGGATTAG 657

Search completed: May 28, 2005, 17:32:03  
Job time : 521 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 28, 2005, 15:06:20 ; Search time 3078 Seconds  
(without alignments)  
8038.264 Million cell updates/sec

Title: US-09-869-566-4  
Perfect score: 650  
Sequence: 1 taattcaccatgtctgcact.....cgactctagagatcccg95 650

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_hic:\*  
4: gb\_esc3:\*  
5: gb\_esc4:\*  
6: gb\_esc5:\*  
7: gb\_esc6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
C 1	493.8	76.0	561	1	AI1343258 tb94b05.X
C 2	431.8	66.4	767	1	BG620449 602617582
C 3	408.8	62.9	485	1	AI1014548 040401.X
C 4	226.2	34.8	372	5	BX283240 BX283240
C 5	225.2	34.6	316	8	AO041691 CIT-HSP-2
6	173	26.6	670	7	CF762015 CBS000784
7	108.6	16.7	624	9	CE135149 tigr-gss-
8	52.4	8.1	299	4	BG271067 tigr-gss-
9	52.4	8.1	342	6	BY793571 BY793571
10	52.4	8.1	363	6	BY768696 BY768696
11	52.4	8.1	382	6	BY771752 BY771752
12	52.4	8.1	500	4	BG270250 tigr-gss-
13	52.4	8.1	527	4	BG270250 tigr-gss-
14	52.4	8.1	550	4	BG270250 tigr-gss-
15	52.4	8.1	550	4	BG270250 tigr-gss-
16	51.4	7.9	466	7	CF581512 AGENCOURT
17	51.2	7.9	1023	6	BY709409 BY709409
18	51.2	7.9	1219	3	AK009787 Mus muscu
19	51	7.8	498	5	BX282030 BX282030
20	50.8	7.8	293	2	BB564808 BB564808
21	50.8	7.8	293	2	BB565124 BB565124
22	50.8	7.8	355	2	BB841364 BB841364
23	50.8	7.8	375	5	BY153883 BY153883
24	50.4	7.8	439	4	BG879138 tigr-gss-

25	50.2	7.7	674	7	CF249061 t63e12.Y
26	49.4	7.6	302	4	BG880282 BG880282
27	49.4	7.6	386	4	BG880018 t63e11.Y
28	49.4	7.6	421	4	BG880821 t63e10.Y
29	49.4	7.6	488	4	BG879799 t63e04.Y
30	49.4	7.6	498	4	BG271014 t63e05.Y
31	49.2	7.6	554	4	BG879105 t63e01.Y
32	49.2	7.6	208	4	BG879931 t63e09.Y
33	49.2	7.6	273	2	BB562774 BB562774
34	49.2	7.6	421	4	BG879296 t63e03.Y
35	49.2	7.6	444	5	BQ126879 t63e10.Y
36	49.2	7.6	513	4	BG879198 t63e06.Y
37	49.2	7.6	820	7	CF578022 AGENCOURT
38	49.2	7.6	831	7	CF581505 AGENCOURT
39	49.2	7.6	843	7	CF581305 AGENCOURT
40	49.2	7.6	873	7	CF581214 AGENCOURT
41	49.2	7.6	893	7	CF580395 AGENCOURT
42	49.2	7.6	904	7	CF585644 AGENCOURT
43	49.2	7.6	971	7	CF581255 AGENCOURT
44	48.6	7.5	379	5	BX283678 BX283678
45	48.6	7.5	684	7	CF249136 t63e01.Y

## ALIGNMENTS

RESULT 1  
LOCUS AI1343258/c  
DEFINITION tb94b05.x1 NCI CGAP Col6 Homo sapiens CDNA clone IMAGE:2061969 3',  
mRNA sequence.  
ACCESSION AI1343258  
VERSION AI1343258.1 GI:4080464  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 561)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Cloned through the I.M.A.G.E. Consortium/HLN at:  
www.bio.lnml.gov/bhrp/image/image.html  
Insert Length: 814 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 471.  
Location/Qualifiers  
1. 561  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2061969"  
/issue\_type="Colon tumor, RER+"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Col6"  
/note="Organ: colon; Vector: pRTT3D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Plasmid DNA from the normalized library NCI CGAP Col6 was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneIDs 1057416-1061255, and 1144584-1145351).





**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Insert length: 1052 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 424.

**FEATURES**

source

1.485  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1628761"  
 /lab\_host="DH10B"  
 /note="Soares NPL T GBC S1"  
 /note="Organ: pooled; Vector: pRT3D-Pac (Pharmacia) with  
 a modified polylinker. Site 1: Not I; Site 2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung, NbH19W, testis NHT, and B-cell  
 NCI CGAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 1 M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

**ORIGIN**

**Query Match** 62.9%; Score 408.8; DB 1; Length 485;  
**Best Local Similarity** 99.5%; Pred. No. 2.2e-113;  
**Matches** 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

215 ACTACATAGCCGAGATCTTCTTGACATTAGCCCTCCTGAGCTCAGCCTCGCGG 274  
 485 ACTACATAGCCGAGATCTTCTTGACATTAGCCCTCCTGAGCTCAGCCTCGCGG 426  
 275 AGAAGAAGAGTCGATCTCTCGGGGCTCTTAAAGGAGTTTGTCTCTACTGTACA 334  
 425 AGAAGAAGAGTCGATCTCTCGGGGCTCTTAAAGGAGTTTGTCTCTACTGTACA 366  
 335 AGGATTAAGGACAACTCATCCCTTCAGCTGAAGAGAAAGTGAAGCTGG 394  
 365 AGGATTAAGGACAACTCATCCCTTCAGCTGAAGAGAAAGTGAAGCTGG 306  
 395 CTGCCCAAAAGAAATGACACCGCCGCTTCATCTTTATAGGGCTCAGGGGCTCT 454  
 305 CTGCCCAAAAGAAATGACACCGCCGCTTCATCTTTATAGGGCTCAGGGGCTCT 246  
 455 GGAACATGCTGAGTGGCGGCTCACCCGAGTGTTCATCTGCACTCTCGCAATTGA 514  
 245 GGAACATGCTGAGTGGCGGCTCACCCGAGTGTTCATCTGCACTCTCGCAATTGA 186  
 515 ATGAGCTTGTGGGCTGACAGATTAATTGAGAAACGAAACATTTGATTTCATTTC 574  
 185 ATGAGCTTGTGGGCTGACAGATTAATTGAGAAACGAAACATTTGATTTCATTTC 126  
 575 AACCAAGTTTGCAAGCTGAATGAGCCCAAGAGGTCAAGCAATTAGAAAC 626  
 125 AACCAAGTTTGCAAGCTGAATGAGCCCAAGAGGTCAAGCAATTAGAAAC 74

**RESULT 4**  
**LOCUS** BX283240 372 bp mRNA linear EST 04-MAR-2003  
**DEFINITION** BX283240 NIH\_MGC\_79 Homo sapiens cDNA clone IMAGE958C221589;  
**IMAGE:** 4731213, mRNA sequence.  
**ACCESSION** BX283240  
**VERSION** BX283240.1 GI:28847694

**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens

**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**AUTHORS** 1 (bases 1 to 372)  
 Ebert, L., Hell, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
 Radloff, U., Schneider, D., and Korn, B.  
**TITLE** Human Unigeneset - RZPD3  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD: [IMAGP958C221589](mailto:IMAGP958C221589).  
 RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
<http://www.rzpd.de/CloneCards/cgl-bin/showLib.pl.cgi/response?libNo=972> Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)

This clone is available royalty-free from RZPD;  
 contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:  
 PCMW-M13u, Primer sequence: CGTTTAAACGACGGCCAGT.

**FEATURES**

source

1.372  
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 /clone\_lib="NIH\_MGC\_79"  
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggccgctcgacc); Site 2: SfiI  
 (ggccatcagcc); 5' and 3' adaptors were used in cloning  
 as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCGC-3'  
 and 3' adaptor sequence:  
 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.3  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC library."

**ORIGIN**

**Query Match** 34.8%; Score 226.2; DB 5; Length 372;  
**Best Local Similarity** 94.7%; Pred. No. 1.4e-57;  
**Matches** 234; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

86 CCGCAATTCAGCTCTTTCAGAGGTCGAAAGGTGAAGACTTAAACCCGAAATTTCA 145  
 126 CCGCATGAATTTTGTTCACAAAGTCCAAAGTGAAGACTTAAACCCGAAATTTCA 185  
 146 GCAATTCAGACCAAGATCAAAAGTACGTGCTGAGCTGGGAATCTCATGAGATTG 205  
 186 GCAATTCAGACCAAGATCAAAAGTACGTGCTGAGCTGGGAATCTCATGAGATTG 245  
 206 CAGATTAATACTACATAGCCGAGAGATCTTCTTGACATTAGCTTCATCTTGAAGTCTGAG 265  
 246 CAGATTAATACTACATAGCCGAGAGATCTTCTTGACATTAGCTTCATCTTGAAGTCTGAG 305  
 266 CCTTGGCGAAGAAAGAGTCCGATTCTCTGGGGGCTCTTAAAGGAGATTGTCTCT 325  
 306 CCTTGGCGAAGAAAGAGTCCGATTCTCTGGGGGCTCTTAAAGGAGATTGTCTCT 365  
 326 ACTGTGA 332  
 366 ACTGTGA 372

**RESULT 5**

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LOCUS A0041691  
DEFINITION CIT-HSP-2326018.TR CIT-HSP Homo sapiens genomic clone 2326018,  
genomic survey sequence.  
ACCESSION A0041691  
VERSION A0041691.1 GI:3310962  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 316)  
Adams,M.D., Kounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,  
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,  
Simon,M. and Venter,J.C.  
Use of a random BAC End Sequence Database for Sequence-Ready Map  
Building (1998)  
Unpublished (1998)  
Other GSSs: CIT-HSP-2326018.TV  
COMMENT Contact: Mark Adams  
Department of Bukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdams@icigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/cdb/hungen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse  
Class: BAC ends.  
FEATURES  
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/cell\_type="Sperm"  
/clone\_lib="CIT-HSP"  
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Query Match 34.6%; Score 225.2; DB 8; Length 316;  
Best Local Similarity 98.7%; Pred. No. 2.7e-57;  
Matches 227; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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DB GCCCAAAAGGAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGG 257  
QY AACATCTGAGTGGCGGCTCAACCGGATGTTATCTGCACTCCCTGCAATTTGTAAT 516  
DB AACATCTGAGTGGCGGCTCAACCGGATGTTATCTGCACTCCCTGCAATTTGTAAT 197  
QY GAGCGTGGGGGTGACAGATAATTGGAACAGAAACACATTGAATTTTCATTCAA 576  
DB GAGCGTGGGGGTGACAGATAATTGGAACAGAAACACATTGAATTTTCATTCAA 137  
QY CCAGTTTGCAAAAGCTGAATGAGCCCGCAGTGAAGTCAAGGATTAGGAAC 626  
DB CCAGTTTGCAAAAGCTGAATGAGCCCGCAGTGAAGTCAAGGATTAGGAAC 87  
RESULT 6  
CF762015 670 bp mRNA linear EST 17-OCT-2003  
LOCUS CF762015  
DEFINITION CCL000784 Bos taurus skin cDNA library Bos taurus cDNA clone  
ACCESSION CF762015  
VERSION CF762015.1 GI:37711233  
KEYWORDS EST.

SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 670)  
Wang,Y.H., McWilliam,S. and Lehnert,S.  
Transcription profiling of cattle skin  
Unpublished (2003)  
COMMENT Contact: Dr Yonghong Wang  
Functional Genomics Lab  
CSIRO Livestock Industries  
Level 5, Queensland Biosciences Precinct, University of Queensland,  
306 Carmody Road St. Lucia QLD Australia  
Tel: 07 3214 2445  
Fax: 07 3214 2685  
Email: Yonghong.Wang@csiro.au  
Plate: 18 row: D column: 12.  
FEATURES  
source  
1. 670  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Hereford Shorthorn"  
/db\_xref="taxon:9913"  
/clone="CCL00784"  
/sex="female"  
/tissue\_type="pooled"  
/dev\_stage="Adult"  
/lab\_host="X11-BluemR",strain"  
/clone\_lib="Bos taurus skin cDNA library"  
/note="Organ: skin; Vector: Uni-ZAPXR; Site\_1: EcoRI;  
Site\_2: Xho I; Library made from pooled skin of adult  
female Hereford-Shorthorn."  
ORIGIN  
Query Match 26.6%; Score 173; DB 7; Length 670;  
Best Local Similarity 62.4%; Pred. No. 3.3e-41;  
Matches 305; Conservative 0; Mismatches 180; Indels 4; Gaps 2;  
QY AGGTCCAAAGGAAGTAAACCTTAACCGAAGAAATTCAGCATTCAGACAGATCACA 167  
DB AGGTCCAAAGGAAGTAAACCTTAACCGAAGAAATTCAGCATTCAGACAGATCACA 243  
QY AGTACTGTCCTGAGACTGTGGAATCTCATAGCAGTTCAGATTAACATACAGCCC 227  
DB AGTACTGTCCTGAGACTGTGGAATCTCATAGCAGTTCAGATTAACATACAGCCC 303  
QY TATTTTGGTCTGAGCTCAGTACCTGAGACAGTTCAGATTAAGATTAAGATCTTCC 287  
DB TATTTTGGTCTGAGCTCAGTACCTGAGACAGTTCAGATTAAGATTAAGATCTTCC 363  
QY AACTACCTAATTATTAATTAATCTCCGAGTGAAGTCAAGTATGAACAAATGATACC 347  
DB AACTACCTAATTATTAATTAATCTCCGAGTGAAGTCAAGTATGAACAAATGATACC 423  
QY GATTCCTCGGGGGTCTCAAGGGAGTGTCTCTACTGACCAAGATTAAGACA 407  
DB GATTCCTCGGGGGTCTCAAGGGAGTGTCTCTACTGACCAAGATTAAGACA 480  
QY AAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAAGCTGGCTCCCAAGGA 467  
DB AAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAAGCTGGCTCCCAAGGA 540  
QY CA---AGCATCCCTGAGCTGAAGACTTAAGAAACCTTCAGACGCTGCCAGAAA 527  
DB CA---AGCATCCCTGAGCTGAAGACTTAAGAAACCTTCAGACGCTGCCAGAAA 600  
QY ATCAGACGCGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGA 587  
DB ATCAGACGCGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGA 659  
QY GGTGACAGATTAATTGGAACAGAAACACATTGAATTTTCATTTCACAGTTTGCA 597  
DB GGTGACAGATTAATTGGAACAGAAACACATTGAATTTTCATTTCACAGTTTGCA 659  
QY ATTG---CAAGATCTCAGATGAAGAGAAACACATGAGTTTCAATTCGGCGCATTA 596  
DB ATTG---CAAGATCTCAGATGAAGAGAAACACATGAGTTTCAATTCGGCGCATTA 596

Db 660 AGCTGAAT 668

RESULT 7  
CE135149

LOCUS CE135149 624 bp DNA linear GSS 25-SEP-2003

DEFINITION tigr-gss-dog-17000326525085 Dog Library Canis familiaris genomic,

ACCESSION CE135149

VERSION CE135149.1 GI:35239139

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 624)

Kirchness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,W., Wang,W., Fraser,C.M. and Venter,J.C.

REFERENCE The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Kirchness EF  
The Institute for Genomic Research  
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirchness@tigr.org  
Class: shotgun.

FEATURES

source

1..624

/organism="Canis familiaris"

/mol\_type="genomic DNA"

/strain="Standard Poodle"

/db\_xref="taxon:9615"

/clone\_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 16.7%; Score 108.6; DB 9; Length 624;  
Best Local Similarity 83.7%; Pred. No. 1.6e-21;  
Matches 123; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 226 CCAGAGATCTTTGATTAAGCTTCATCTTGAGCTCAGCTTCGAGGAGAAAGAACT 285

Db 247 CCAGAGATCTTTGATTAAGCTTCATCTTGAGCTCAGCTTCGAGGAGAAAGAACT 306

QY 286 CGATTTCTCTGGGGCTCTCTAAAGGAGATTGCTCTACTGTGACAAAGATAAGCA 345

Db 307 CCAATTCCTTTGGCACTGTGAAGAGAGCTTTGCTCTGTGTGAAGAGACAGAGA 366

QY 346 CAAAGTCATCATCCCTTCAGCTGAAG 372

Db 367 CAAAGCCACATCTTCAGCTGAAG 393

RESULT 8  
BG271067

LOCUS BG271067 299 bp mRNA linear EST 13-MAR-2002

DEFINITION IBOH11.Y1 Melton Mouse Adult Pancreas 1 Mus musculus cDNA clone IMAGE:5646957 5', similar to SW:TRYP\_MOUSE P07146 TRYPSINOGEN PRECURSOR ;, mRNA sequence.

ACCESSION BG271067

VERSION BG271067.1 GI:12978839

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 299)

AUTHORS

Melton,D., Meadows,A., Clifton,S., Hallier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blistein,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagariswilli,R., Williams,T., Jackson,Y. and Bowers,Y.

Washu-Harvard Pancreas EST Project

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)

MGI:1851677 This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov

Seq primer: -40RP from Gibco

High quality sequence stop: 292.

Location/Qualifiers

1..299

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="ICR"

/db\_xref="taxon:10090"

/clone="IMAGE:5646957"

/sex="Male"

/tissue.type="Total Pancreas"

/dev\_stage="Adult"

/lab\_host="TOP10"

/clone\_lib="Melton Mouse Adult Pancreas 1"

/note="Organ: Pancreas; Vector: pZeo-2; Site 1: Not I; Site 2: Xho I; Library constructed using SuperScript plasmid library kit (Life Technologies). cDNA made by oligo-dT priming. Xho I site destroyed during cloning. Size-selected by column fractionation. Primary library, unamplified."

ORIGIN

Query Match 8.1%; Score 52.4; DB 4; Length 299;  
Best Local Similarity 79.5%; Pred. No. 0.00019;  
Matches 62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 5 TCACATGTCGACATTCATCTAGCTCTGTTGAGAGCTCAGTGTGACTACAAG 64

Db 23 TCACATGATGACATCTTCATCTAGCTCTGTTGAGAGCTCTGTTCCTCCGTGG 82

QY 65 ACATGACGACAAAGCTTG 82

Db 83 ATGATGATGACAAAGATTG 100

RESULT 9  
BY793571

LOCUS BY793571 342 bp mRNA linear EST 23-MAR-2004

DEFINITION BY793571 RIKEN full-length enriched, 17.5 days embryo whole body Mus musculus cDNA clone L930285A07 5', mRNA sequence.

ACCESSION BY793571

VERSION BY793571.1 GI:39720210

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 342)

Carninci,P., Waki,K., Shiraki,T., Konno,H., Shibata,K., Itoh,M., Aizawa,K., Arikawa,T., Ishii,Y., Sasaki,D., Bono,H., Kondo,S., Sugahara,Y., Saito,R., Osato,N., Fukuda,S., Sato,K., Watabiki,A., Hirozane-Kishikawa,T., Nakamura,M., Shibata,Y., Yasunishi,A.,

TITLE	JOURNAL MEDLINE PUBMED			
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.jp/) for further details.			
FEATURES	Location/Qualifiers 1..342 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="L930285A07" /tissue_type="whole body" /dev_stage="17.5 days embryo" /clone_id="RIKEN full-length enriched, 17.5 days embryo whole body"			
ORIGIN	Query Match 8.1%; Score 52.4; DB 6; Length 342; Best Local Similarity 79.5%; Pred. No. 0.0002; Matches 62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;			
Oy	5 TCACCATGTCGCACTTGTGATCCTGAGCTGTTGTTGAGCGTGCAGTCTCTACATCAAG 64       Db 11 TCACCATGAGCGCACTTGTGATCCTGAGCGTCTTGTGAGCGTGCAGTCTCTCTG 70 			
Oy	65 ACGATGACGACAGCGTTG 82       Db 71 ATGATGATGACAGGATTG 88 			
RESULT 10	BY768696 363 bp mRNA linear EST 22-MAR-2004			
LOCUS	BY768696 RIKEN full-length enriched, 17.5 days embryo whole body			
DEFINITION	Mus musculus cDNA clone L930023M20 5', mRNA sequence.			
ACCESSION	BY768696			
VERSION	BY768696.1 GI:39693687			
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 363)			
AUTHORS	Carninci, P., Waki, K., Shiraki, T., Kono, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, T., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watanishi, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kiyama, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aldins, V., Nakagawa, A., Heid, W. A., Iwata, H., Kono, T., Nakachi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Murai, T. M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.			

TITLE	Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
JOURNAL MEDLINE	Genome Res. 13 (6B), 1273-1289 (2003)
PUBMED	12819125
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute the Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216 Fax: 81-45-503-9226 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site ( <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> ) for further details.
FEATURES	Location/Qualifiers
source	1. 363 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="1930023M20" /tissue_type="whole body" /dev_stage="17.5 days embryo" /clone_1lb="RIKEN full-length enriched, 17.5 days embryo whole body"
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Query Match	8.1%; Score 52.4; DB 6; Length 363;
Best Local Similarity	79.5%; Pred. No. 0.00021;
Matches	62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY	5 TCACCAATGCTGCACCTTCTGATCTTACTCTTTGTGGAGCTGCAGTCTGACTACAAAG 64
Db	11 TCACCAATGAGGACGACCTTCTGATCTTACTACCCCTTGGAGAGCTGCTGTTCCCTGTGG 70
QY	65 ACGATGACGACCAAGCTTG 82
Db	71 ATGATGATGACACAGATTG 88
RESULT 11	
BY771752	382 bp mRNA linear EST 23-MAR-2004
LOCUS	BY771752 RIKEN full-length enriched, 17.5 days embryo whole body
DEFINITION	Mus musculus cDNA clone J930056N12 5', mRNA sequence.
ACCESSION	BY771752
VERSION	BY771752.1 GI:39698390
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 382)
AUTHORS	Carninci, P., Waki, K., Shiraki, T., Kono, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watanahki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kituchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavani, M., Aldini, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Ozanski, Y., Kawai, J. and Hayashizaki, Y.
TITLE	Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
JOURNAL MEDLINE	Genome Res. 13 (6B), 1273-1289 (2003)
PUBMED	12819125

**COMMENT**  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site (http://genome.gsc.riken.jp/) for  
 further details.

**FEATURES**  
 source  
 1..382  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
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 /dev\_stage="17.5 days embryo"  
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 whole body"

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 Best Local Similarity 79.5%; Pred. No. 0.00021;  
 Matches 62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 5 TCACCATGTCGACCTTGATCTGATCTGCTGTTGGAGCTGCAGTGTGCTGATCAAGA 64  
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 Db 11 TCACCATGATGACCTTGATCTGATCTGATCCCTTGAGAGCTGCTGTGCTTCCCTG 70  
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 Qy 65 ACATGACGACCAAGCTTG 82  
 |||||  
 Db 71 ATGATGATGACCAAGATTG 88  
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**RESULT 12**  
 BG270250 500 bp mRNA linear EST 13-MAR-2002  
 Iblia12.y1 Melton Mouse Adult Pancreas 2 Mus musculus cDNA clone  
 IMAGE:5647391 5' similar to SW:TRYP\_MOUSE P07146 TRYPSINOGEN  
 PRECURSOR ;, mRNA sequence.

**ACCESSION**  
 BG270250  
**VERSION**  
 BG270250.1 GI:12977197  
**KEYWORDS**  
 EST.  
**SOURCE**  
 Mus musculus (house mouse)  
**ORGANISM**  
 Mus musculus  
**REFERENCE**  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 500)  
 Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,  
 Wylie,T., Martin,J., Blistein,A., Schmitt,A., Theising,B.,  
 Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,  
 McCann,R., Cole,R., Tsagaratshvili,R., Williams,T., Jackson,Y. and  
 Bowers,Y.  
 WashU-Harvard Pancreas EST Project  
 Unpublished (2000)  
**TITLE**  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Juliana Brown

(brown@fas.harvard.edu)  
 MGI:185411 This sequence now available from the IMAGE consortium,  
 for clone orders contact: info@image.llnl.gov  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 491.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
 /clone="IMAGE:5647391"  
 /sex="Male"  
 /tissue\_type="Total Pancreas"  
 /dev\_stage="Adult"  
 /lab\_host="TOP10"  
 /clone\_lib="Melton Mouse Adult Pancreas 2"  
 /note="Organ: Pancreas; Vector: pZEXO-2; Site 1: Not I;  
 Site 2: Xho I; Library constructed using Superscript  
 Plasmid Library kit (Life Technologies). cDNA made by  
 oligo-dT priming. Xho I site destroyed during cloning.  
 Size-selected by column fractionation. Primary library,  
 unamplified."

**ORIGIN**  
 Query Match 8.1%; Score 52.4; DB 4; Length 500;  
 Best Local Similarity 79.5%; Pred. No. 0.00023;  
 Matches 62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 5 TCACCATGTCGACCTTGATCTGATCTGCTGTTGGAGCTGCAGTGTGCTGATCAAGA 64  
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 Db 7 TCACCATGATGACCTTGATCTGATCTGATCCCTTGAGAGCTGCTGTGCTTCCCTG 66  
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 Qy 65 ACATGACGACCAAGCTTG 82  
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 Db 67 ATGATGATGACCAAGATTG 84  
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**RESULT 13**  
 BG270248 527 bp mRNA linear EST 13-MAR-2002  
 Iblia09.y1 Melton Mouse Adult Pancreas 2 Mus musculus cDNA clone  
 IMAGE:5647385 5' similar to SW:TRYP\_MOUSE P07146 TRYPSINOGEN  
 PRECURSOR ;, mRNA sequence.

**ACCESSION**  
 BG270248  
**VERSION**  
 BG270248.1 GI:12977193  
**KEYWORDS**  
 EST.  
**SOURCE**  
 Mus musculus (house mouse)  
**ORGANISM**  
 Mus musculus  
**REFERENCE**  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 527)  
 Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,  
 Wylie,T., Martin,J., Blistein,A., Schmitt,A., Theising,B.,  
 Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,  
 McCann,R., Cole,R., Tsagaratshvili,R., Williams,T., Jackson,Y. and  
 Bowers,Y.  
 WashU-Harvard Pancreas EST Project  
 Unpublished (2000)  
**TITLE**  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Juliana Brown  
 (brown@fas.harvard.edu)  
 MGI:1854105 This sequence now available from the IMAGE consortium,  
 for clone orders contact: info@image.llnl.gov

Seq primer: -40RP from Gibco  
High quality sequence stop: 509.

## FEATURES

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1. .527
/organism="Mus musculus"
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/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5647385"
/sex="Male"
/tissue_type="Total Pancreas"
/dev_stage="Adult"
/lab_host="TOP10"
/clone_lib="Melton Mouse Adult Pancreas 2"
/notes="Organ: Pancreas; Vector: pZERO-2; Site_1: Not I; Site_2: Xho I library constructed using SuperScript Plasmid library kit (Life Technologies). cDNA made by oligo-dt priming. Xho I site destroyed during cloning. Size selected by column fractionation. Primary library unamplified."

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**ORIGIN**

Query Match	8.1%	Score 52.4;	DB 4;	Length 527;
Best Local Similarity	79.5%;	Pred. No. 0.00023;		
Matches	62;	Mismatches	16;	Indels 0;
		Gaps	0;	

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		TCACCAAGTCTGCACCTCTGATCCGACCTTGTGTGAGCTGCAGATGCTGACAAAG	6
Db	7	TCACCAAGAGTGACCTCTGATCCTACCCCTGTGGAGCTGCTGTTCCCTGTGG	6
Oy	65	ACGATGACGACAAAGCTTG	82
Db	67	ATGATGATGACAAAGATTG	84

**source**

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1. .650
/organism="Mus musculus"
/mol_type="mrna"
/strain="ICR"
/db_xref="taxon:10090"
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/sex="Male"
/tissue_type="Total Pancreas"
/dev_stage="Adult"
/lab_host="TOP10"
/clone_1b="Wetlcon Mouse Adult Pancreas 2"
/notes="Organ: Pancreas; Vector: pZEO-2; Site_1: Not I;
Site_2: Xho I; library constructed using SuperScript
Plasmid Library kit (Life Technologies). cDNA made by
oligo-dT priming. Xho I site destroyed during cloning.
Size-selected by column fractionation. Primary library
unamplified."

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ORIGIN

Query Match	8.1%	Score 52.4	DB 4	Length 650
Best Local Similarity	79.5%	Pred. No. 0.00025		
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Oy 5 TCACCAATGTCGACACTTCATCTCATCTTGTGAGCTGCAGTGTGCACTAACAAAG 64  
 Db 7 TCACCAAGATGACACTTCATCTCATCTTGTGAGAGTGTGCTGTGCTTCCCTGTG 66  
 Oy 65 ACGATGACGACAAAGCTTG 82  
 Db 67 ATGATGATGACAAAGATTG 84

Search completed: May 28, 2005, 17:20:20  
Job time : 3082 secs

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